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197582

Fr m: Ramirez, Delia
S nt: Thursday, August 03, 2006 4:56 PM
To: STIC-Biotech/ChemLib
Subject: 10/612779

Hi,

I would like to request the following search: SEQ ID NO:2 in the protein databases.

Please provide a printout of this search.

Thank you very much,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70
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Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 7, 2006, 09:20:34 ; Search time 92 Seconds
(without alignments)
3026.574 Million cell updates/sec

Title: US-10-612-779-2

Perfect score: 3086

Sequence: 1 MCGIVGAIQRDVAEILLEG.....LRGTVDQPRNLAKSVTVE 609

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_8:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

9: Geneseq2005s:*

10: Geneseq2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3086	100.0	609	3	AAV58822 E. coli g
2	3086	100.0	609	4	AAU34806 E. coli c
3	3086	100.0	609	6	ABU28829 Protein e
4	3086	100.0	609	8	ADI38857 Glucosami
5	3086	100.0	609	8	ADS45181 Bacterial
6	3086	100.0	609	8	ADU00590 Amino aci
7	3081	99.8	608	9	ADW23840 Novel hum
8	3080	99.8	609	3	AAV58827 E. coli g
9	3080	99.8	609	3	AAV58826 E. coli g
10	3080	99.8	609	8	ADI38865 Mutant gl
11	3080	99.8	609	8	ADI38867 Mutant gl
12	3079	99.8	609	3	AAV58825 E. coli g
13	3079	99.8	609	8	ADI38863 Mutant gl
14	3071	99.5	609	3	AAV58823 E. coli g
15	3071	99.5	609	8	ADI38859 Mutant gl
16	3068	99.4	609	3	AAV58824 E. coli g
17	3068	99.4	609	8	ADI38861 Mutant gl
18	3068	99.4	609	8	ADU00592 Amino aci
19	3061	99.2	609	8	ADI38869 Mutant gl
20	3053	98.9	609	4	AAU38472 Salmonell
21	3053	98.9	609	6	ABU48228 Protein e
22	2950	95.6	609	6	ABU28355 Protein e
23	2876	93.2	609	4	AAU36165 Klebsiell

24	2876	93.2	651	7	ABO64174 Klebsiell
25	2871	93.0	609	6	ABU31411 Protein e
26	2718.5	88.1	608	6	ABU45041 Protein e
27	2682	86.9	609	6	ABU50609 Protein e
28	2661	86.2	609	8	ADS42812 Bacterial
29	2619	84.9	609	8	ADN17785 Bacterial
30	2570	83.3	610	6	ABM70565 Photothab
31	2510.5	81.4	622	7	ADF07237 Bacterial
32	2505.5	81.2	608	6	ABU41104 Protein e
33	2270.5	73.6	610	4	AAU35425 Haemophil
34	2270.5	73.6	610	6	ABU30239 Protein e
35	2270.5	73.6	610	6	AAE30459 Haemophil
36	2270.5	73.6	610	10	AAE31344 Haemophil
37	2264.5	73.4	610	6	ABU49139 Protein e
38	2202.5	71.4	610	6	ABU39464 Protein e
39	2007	65.0	611	6	ABU39730 Protein e
40	2002.5	64.9	610	8	ADS24814 Bacterial
41	1995	64.6	611	4	AAU36518 Pseudomon
42	1995	64.6	611	6	ABU38924 Protein e
43	1995	64.6	616	7	ABO70418 Pseudomon
44	1987	64.4	611	6	ABU41714 Protein e
45	1806.5	58.5	612	6	ABU17019 Protein e

ALIGNMENTS

RESULT 1

AAV58822 ID AAY58822 standard; protein; 609 AA.

XX AC AAY58822;

XX DT 08-MAY-2000 (first entry)

XX DE E. coli glucosamine-6-phosphate synthase.

XX KW Glucosamine-6-phosphate synthase; GlcN6P; glucosamine;

XX KM metabolic engineering; plasmid pKLN23-28.

XX OS Escherichia coli.

XX WO200004182-A1.

XX PN 27-JAN-2000.

XX PD 15-JUL-1999; 99WO-US015976.

XX PR 15-JUL-1998; 98US-00115475.

XX (DCVB-) DCV INC DBA BIO-TECH RESOURCES.

XX PI Berry A, Burlingame RP, Millis JR;

XX WPI; 2000-182441/16.

XX DR N-PSDB; AAZ58249.

XX PT Fermentation of E. coli having an altered amino acid sugar metabolic pathway to produce glucosamine, especially using novel recombinant variant glucosamine-6-phosphate synthases.

XX PS Claim 15; Page 111-113; 150pp; English.

XX CC The present sequence is that of wild-type glucosamine-6-phosphate synthase (GlcN6P synthase) of Escherichia coli strain W3110. The sequence is predicted from the isolated glms gene (see AAZ58249) in plasmid pKLN23-28. Recombinant nucleic acids encoding GlcN6P synthase are claimed, and are used for the expression of the enzyme in host microbial strains, especially E. coli, for use in the production of glucosamine. The invention also provides methods for the overproduction of glucosamine using a genetically engineered microorganism that encodes a GlcN6P synthase modified to increase its activity (see also AAY58823-27). Preferred modifications comprise amino acid deletion, insertion,

CC inversion, derivatisation or substitution, especially I4T, I272T, S240P,
XX A39T, R250C, G472S and L469P substitution, of the present sequence
SQ Sequence 609 AA;

Query Match 100.0%; Score 3086; DB 3; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.7e-264;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCGIVGAIAQRDVAEILLEGRLLEYRGYDSAGLAVVDAEGHTRRLRLGKVQMLAQAAE 60
Db 1 MCGIVGAIAQRDVAEILLEGRLLEYRGYDSAGLAVVDAEGHTRRLRLGKVQMLAQAAE 60
Qy 61 EHPHGGTGIATRWATHGEPSEVNAHPVSEHVVVHNGIIEHNHPLREELKARGYTFV 120
Db 61 EHPHGGTGIATRWATHGEPSEVNAHPVSEHVVVHNGIIEHNHPLREELKARGYTFV 120
Qy 121 SETDTEVIAHLVNNELKQGGLTREAVALRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNNELKQGGLTREAVALRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Qy 181 IGLGMGENFIASDQALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRODIESNLQ 240
Db 181 IGLGMGENFIASDQALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRODIESNLQ 240
Qy 241 YDAGDKGIYRHYMQEYEQPNAIKNTLTGRISHGQVDLSSELGNADLLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQEYEQPNAIKNTLTGRISHGQVDLSSELGNADLLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFRRYKSAVRNSLMITLSQSGETADTLA 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFRRYKSAVRNSLMITLSQSGETADTLA 360
Qy 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFITQTLVLLMLVAKL 420
Db 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFITQTLVLLMLVAKL 420
Qy 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSDKRIEALAEFSDKHAFILGRGDQYPTA 480
Db 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSDKRIEALAEFSDKHAFILGRGDQYPTA 480
Qy 481 LEGALKLKEISYTHABAYAGELKHGFLALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
Db 481 LEGALKLKEISYTHABAYAGELKHGFLALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
Qy 541 GGOLYVFADQDAGFVSSDNNHIIEMPHVEVIAPIETVPLQLLAYHVALIKGTDVQPR 600
Db 541 GGOLYVFADQDAGFVSSDNNHIIEMPHVEVIAPIETVPLQLLAYHVALIKGTDVQPR 600
Qy 601 NLAQSVTVE 609
Db 601 NLAQSVTVE 609

RESULT 2
AAU34806
ID AAU34806 standard; protein; 609 AA.
XX
AC AAU34806;
XX
DT 14-FEB-2002 (first entry)
XX
DE E. coli cellular proliferation protein #387.
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX
OS Escherichia coli.
XX
PN W0200170955-A2.
XX
PD 27-SEP-2001.
XX

PF 21-MAR-2001; 2001WO-US009180..
XX
PR 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-020727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Haselbeck R, Ohlgen KL, Zyskind JW, Wall D, Trawick JD, Carr GU;
PI Yamamoto RT, Xu HH;
XX
DR WPI; 2001-611495/70.
DR N-PSDB; AAS52665.
XX
PT New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids.
PS Example 3; SEQ ID NO 10399; Silpp; English.
CC
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes,
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 609 AA;

Query Match 100.0%; Score 3086; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.7e-264;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCGIVGAIAQRDVAEILLEGRLLEYRGYDSAGLAVVDAEGHTRRLRLGKVQMLAQAAE 60
Db 1 MCGIVGAIAQRDVAEILLEGRLLEYRGYDSAGLAVVDAEGHTRRLRLGKVQMLAQAAE 60
Qy 61 EHPHGGTGIATRWATHGEPSEVNAHPVSEHVVVHNGIIEHNHPLREELKARGYTFV 120
Db 61 EHPHGGTGIATRWATHGEPSEVNAHPVSEHVVVHNGIIEHNHPLREELKARGYTFV 120
Qy 121 SETDTEVIAHLVNNELKQGGLTREAVALRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNNELKQGGLTREAVALRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Qy 181 IGLGMGENFIASDQALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRODIESNLQ 240
Db 181 IGLGMGENFIASDQALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRODIESNLQ 240
Qy 241 YDAGDKGIYRHYMQEYEQPNAIKNTLTGRISHGQVDLSSELGNADLLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQEYEQPNAIKNTLTGRISHGQVDLSSELGNADLLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFRRYKSAVRNSLMITLSQSGETADTLA 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFRRYKSAVRNSLMITLSQSGETADTLA 360
Qy 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFITQTLVLLMLVAKL 420

Db 361 RLKGLDASIEHDIVHGLQALPSRIEQMLSDQKRIEALAEFSDKHHALFLGRGDQYPIA 480
Qy 421 SRLKGLDASIEHDIVHGLQALPSRIEQMLSDQKRIEALAEFSDKHHALFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDIVHGLQALPSRIEQMLSDQKRIEALAEFSDKHHALFLGRGDQYPIA 480
Qy 481 LEGALKLKEISYTHAEAYAGELKHGFLALIDADMPVIVVAPNNLEKLSNIEEVRAR 540
Db 481 LEGALKLKEISYTHAEAYAGELKHGFLALIDADMPVIVVAPNNLEKLSNIEEVRAR 540
Qy 541 GGQLYVPADQDAGFVSSDNNHIIEMPHVEEVIAPFTVTPQLLAYHVALIKGTVDVQPR 600
Db 541 GGQLYVPADQDAGFVSSDNNHIIEMPHVEEVIAPFTVTPQLLAYHVALIKGTVDVQPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 3
ABU28829
ID ABU28829 standard; protein; 609 AA.
AC ABU28829;
XX
XX 19-JUN-2003 (first entry)
XX Protein encoded by Prokaryotic essential gene #14356.
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX Escherichia coli.
XX WQ020277183-A2.
XX 03-OCT-2002.
XX 21-MAR-2002; 2002WO-US009107.
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX (BLIT-) ELITRA PHARM INC.
PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
PI WPI; 2003-029926/02.
DR N-PSDB; ACA32699.
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX Claim 25; SEQ ID NO 56753; 1766pp; English.
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 609 AA;
Query Match 100.0%; Score 3086; DB 6; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.7e-264;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MCGIVGAIARDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRRLRGKVMQAQAAE 60
Db 1 MCGIVGAIARDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRRLRGKVMQAQAAE 60
Qy 61 EPHLGGTGTAHTRWATHGEPSEVNAHPHVSEHIVVHNGIIEHNEPLREELKARGYTFV 120
Db 61 EPHLGGTGTAHTRWATHGEPSEVNAHPHVSEHIVVHNGIIEHNEPLREELKARGYTFV 120
Qy 121 SETDTEVIAHLNVNWLKQGGTLREAVLRAIPQURGAYGTVMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLNVNWLKQGGTLREAVLRAIPQURGAYGTVMDSRHPDTLLAARSGSPLV 180
Qy 181 IGLGMENFIASDQALLPVTRRFIFLEEGDIAEITRRSVNI FDKTGAEVKRDIESNLQ 240
Db 181 IGLGMENFIASDQALLPVTRRFIFLEEGDIAEITRRSVNI FDKTGAEVKRDIESNLQ 240
Qy 241 YDAGDKGIVRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSELGNADLLSKVEHIQILA 300
Db 241 YDAGDKGIVRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSELGNADLLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFEFRYKSAVRNSLMTLSQSGETADTLA 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFEFRYKSAVRNSLMTLSQSGETADTLA 360
Qy 361 RLSKELGYLGSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAPTTLTLLMLVAKL 420
Db 361 RLSKELGYLGSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAPTTLTLLMLVAKL 420
Qy 421 SRLKGLDASIEHDIVHGLQALPSRIEQMLSDQKRIEALAEFSDKHHALFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDIVHGLQALPSRIEQMLSDQKRIEALAEFSDKHHALFLGRGDQYPIA 480
Qy 481 LEGALKLKEISYTHAEAYAGELKHGFLALIDADMPVIVVAPNNLEKLSNIEEVRAR 540
Db 481 LEGALKLKEISYTHAEAYAGELKHGFLALIDADMPVIVVAPNNLEKLSNIEEVRAR 540
Qy 541 GGQLYVPADQDAGFVSSDNNHIIEMPHVEEVIAPFTVTPQLLAYHVALIKGTVDVQPR 600
Db 541 GGQLYVPADQDAGFVSSDNNHIIEMPHVEEVIAPFTVTPQLLAYHVALIKGTVDVQPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609
RESULT 4
ADI38857
ID ADI38857 standard; protein; 609 AA.

XX
AC ADI38857;
DT 15-APR-2004 (first entry)
XX
DE Glucosamine-6-phosphate synthase, glms, SEQ ID 2.
XX
KW Glucosamine; N-acetylglucosamine; fermentation;
KW Glucosamine-6-phosphate acetyltransferase;
KW Glucosamine-6-phosphate synthase; Glucosamine-6-phosphate deaminase;
KW Glucosamine-1-phosphate N-acetyltransferase; Glucosamine-6-phosphate;
KW Glucosamine-1-phosphate; N-acetylglucosamine-1-phosphate;
KW N-acetylglucosamine-6-phosphate; enzyme.
XX
OS Escherichia coli.
XX
XX WO2004003175-A2.
XX
XX 08-JAN-2004.
XX
XX 01-JUL-2003; 2003WO-US020925.
XX
XX 01-JUL-2002; 2002US-0393348P.
XX
XX (ARKI-) ARKION LIFE SCI LLC.
XX
XX Deng M, Angerer JD, Cyron D, Grund AD, Jerrell TA, Leanna C;
XX Mathre O, Rosson R, Running J, Severson D, Song L, Wassink S;
XX
XX WPI; 2004-203380/19.
XX
XX N-PSDB; ADI38856.
XX
XX Producing glucosamine or N-acetylglucosamine by fermentation involves
XX culturing microorganism comprising glucosamine-6-phosphate
XX acetyltransferase, in fermentation medium, and collecting product.
XX
XX Claim 15; SEQ ID NO 2; 327pp; English.
XX
XX The present invention relates to a method (M1) for producing glucosamine
XX and N-acetylglucosamine by fermentation. The method comprises (a)
XX culturing in a fermentation medium a microorganism (I) which comprises
XX endogenous glucosamine-6-phosphate acetyltransferase (II) and a genetic
XX modification that increases the activity of (II), glucosamine-6-phosphate
XX synthase (III) or glucosamine-6-phosphate deaminase (IV), or decreases
XX the activity of (IV) and increases the activity of glucosamine-1-
XX phosphate N-acetyltransferase (V), and (b) and collecting the product,
XX which is chosen from the group consisting of glucosamine-6-phosphate,
XX glucosamine, glucosamine-1-phosphate, N-acetylglucosamine-1-phosphate, N-
XX acetylglucosamine-6-phosphate, and N-acetylglucosamine. The present
XX sequence was used to illustrate the method of the invention.
XX
SQ Sequence 609 AA;
Query Match 100.0%; Score 3086; DB 8; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.7e-264;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCGIVGAIARDVAEILLEGRLRLEVRGYDSAGLAVVDAEGHMTLRRLRGKQVQLAAAE 60
DB 1 MCGIVGAIARDVAEILLEGRLRLEVRGYDSAGLAVVDAEGHMTLRRLRGKQVQLAAAE 60
QY 61 EHPHGGTGIAHTRWATHGEPSEVNAPHVSEHVVVHNGIENHEPLREELKARGYTFV 120
DB 61 EHPHGGTGIAHTRWATHGEPSEVNAPHVSEHVVVHNGIENHEPLREELKARGYTFV 120
QY 121 SETDTEVIAHVNWELKQGTLEAVLRAIPOLRGAYGTIVMDSRHPDTLLAARSGSLV 180
DB 121 SETDTEVIAHVNWELKQGTLEAVLRAIPOLRGAYGTIVMDSRHPDTLLAARSGSLV 180
QY 181 IGLGMGENFIASDQALLPVTRFRFLEEGDIAETTRRSVNI FDKTGAEVKRODIESNLQ 240
DB 181 IGLGMGENFIASDQALLPVTRFRFLEEGDIAETTRRSVNI FDKTGAEVKRODIESNLQ 240

QY 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADLLSKVEHIQILA 300
DB 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADLLSKVEHIQILA 300
QY 301 CGTSYNSGMVSRYPFESLAGIPCDEVEIASFPRYKSAVRNLSMITLSQSGTADTLAGL 360
DB 301 CGTSYNSGMVSRYPFESLAGIPCDEVEIASFPRYKSAVRNLSMITLSQSGTADTLAGL 360
QY 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQLTVLLMLVAKL 420
DB 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQLTVLLMLVAKL 420
QY 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSQDKRIEALAEFSDKHAFALFGRGQYPIA 480
DB 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSQDKRIEALAEFSDKHAFALFGRGQYPIA 480
QY 481 LEGALKLKEISYIHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEEVRAR 540
DB 481 LEGALKLKEISYIHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEEVRAR 540
QY 541 GGQLYVFADQDAGFVSSDNMHIEMPHVEEVIPIFYTVPLQLLAYHVALIKGTDVQDPR 600
DB 541 GGQLYVFADQDAGFVSSDNMHIEMPHVEEVIPIFYTVPLQLLAYHVALIKGTDVQDPR 600
QY 601 NLAKSVTVVE 609
DB 601 NLAKSVTVVE 609
RESULT 5
ADS45181
ID ADS45181 standard; protein; 609 AA.
XX
AC ADS45181;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #23611.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
OS Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 23611; 122pp; English.
XX

CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transforming plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 609 AA;

Query Match 100.0%; Score 3086; DB 8; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.7e-264;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCGIVGAIARDVAEILLEGRLRLEYRGYDSAGLAVVDAGHMTLRRLRGKVMQAQAAE 60
DB 1 MCGIVGAIARDVAEILLEGRLRLEYRGYDSAGLAVVDAGHMTLRRLRGKVMQAQAAE 60
QY 61 EHPLHGCGTGAHTRWATHGPSEVNAHPHYSEHIVVHNGIENHEPLRELKARGYTFV 120
DB 61 EHPLHGCGTGAHTRWATHGPSEVNAHPHYSEHIVVHNGIENHEPLRELKARGYTFV 120
QY 121 SETDTEVIAHLVNWELKQGTLEAVLRAIPOLRGAYGTVMDSRHPDTHLAARSGSPLV 180
DB 121 SETDTEVIAHLVNWELKQGTLEAVLRAIPOLRGAYGTVMDSRHPDTHLAARSGSPLV 180
QY 181 IGLGMGNFTASDQALLPVTTRRIFLEEGDIAETRISVNIPOKTAEGVKRODIESNLQ 240
DB 181 IGLGMGNFTASDQALLPVTTRRIFLEEGDIAETRISVNIPOKTAEGVKRODIESNLQ 240
QY 241 YDAGDKGIYRHYMQEYEQPNAIKNTLTGRISHGQVDLSSELGNADLLSKVEHIQILA 300
DB 241 YDAGDKGIYRHYMQEYEQPNAIKNTLTGRISHGQVDLSSELGNADLLSKVEHIQILA 300
QY 301 CGTSYNGMSRYWFESLAGIPCDVEIASBFRYKSAVRNSLMTLSQSGETADTLA 360
DB 301 CGTSYNGMSRYWFESLAGIPCDVEIASBFRYKSAVRNSLMTLSQSGETADTLA 360
QY 361 RLSKELGYLSLALCNVPGSSLVRESLALMTNAGTEIGVASTKFTTQLTVLLMLVAKL 420
DB 361 RLSKELGYLSLALCNVPGSSLVRESLALMTNAGTEIGVASTKFTTQLTVLLMLVAKL 420
QY 421 SRLKGLDASIEHDIVHGLQALPSRIEQLMSQDKRIEALAEFDSKXHALFLGRGDQYPIA 480
DB 421 SRLKGLDASIEHDIVHGLQALPSRIEQLMSQDKRIEALAEFDSKXHALFLGRGDQYPIA 480
QY 481 LEGALKUKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNLEKUKSNIIEVVRAR 540
DB 481 LEGALKUKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNLEKUKSNIIEVVRAR 540
QY 541 GGQLYVFADQDAGFVSSDNNHIIEMPHVEEVIAPFVTVPLQLLAYHVALIKGTDVDDQR 600
DB 541 GGQLYVFADQDAGFVSSDNNHIIEMPHVEEVIAPFVTVPLQLLAYHVALIKGTDVDDQR 600
QY 601 NLAKSVTVE 609
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DB 601 NLAKSVTVE 609
RESULT 6
ADU00590
ID ADU00590 standard; protein; 609 AA.
XX AC ADU00590;
DT 13-JAN-2005 (first entry)
XX DE Amino acid sequence of a glucosamine-6-phosphate synthase.
XX KW chitin; chitosan; fermentation;
KW glutamine-fructose-6-phosphate amidotransferase; glucosamine synthetase;
KW glucosamine-6-phosphate synthase; GPAL gene; glms gene;
KW glucosamine-6-phosphate acetyltransferase; GNA1 gene; chitin synthase;
KW chitin deacetylase; CDAL gene; CDA2 gene;
KW N-acetylglucosamine-6-phosphate deacetylase;
KW glucosamine-6-phosphate deaminase; chitinase; chitosanase; fungus; yeast;
KW enzyme.
XX OS Escherichia coli.
XX PN WO2004092391-A2.
XX PD 28-OCT-2004.
XX PF 12-APR-2004; 2004WO-US011286.
XX PR 11-APR-2003; 2003US-0462087P.
XX PA (ARKI-) ARKION LIFE SCI LLC.
XX PI Deng M, McMullin TW, Grund AD;
XX WPI; 2004-766880/75.
XX DR N-PSDB; ADU00589.
XX PT Producing chitin or chitosan, involves culturing microorganism with
PT genetic modification that results in increase in activity of glutamine-
PT fructose-6-phosphate amidotransferase, in fermentation medium, to produce
PT chitin or chitosan.
XX Example 1; SEQ ID NO 23; 161pp; English.
XX CC The specification describes a method for producing chitin or chitosan by
CC a fermentation process. The method involves culturing in a fermentation
CC medium a microorganism which comprises one or more genetic modifications
CC that result in an increase in the activity of glutamine-fructose-6-
CC phosphate amidotransferase (also known as glucosamine synthetase and
CC glucosamine-6-phosphate synthase, and encoded by the GPAL eukaryotic gene
CC and the glms bacterial gene), glucosamine-6-phosphate acetyltransferase
CC (encoded by GNA1), chitin synthase or chitin deacetylase (encoded by CDAL
CC and CDA2), or in decrease in the activity of N-acetylglucosamine-6-
CC phosphate deacetylase, glucosamine-6-phosphate deaminase, chitinase and
CC chitosanase, and collecting the chitin or chitosan. The method is useful
CC for producing chitin or chitosan by utilizing microorganisms such as
CC fungus, yeast (e.g. Saccharomyces or Schizosaccharomyces) and
CC filamentous fungus (e.g. Aspergillus, Absidia or Rhizopus), preferably S.
CC cerevisiae, A. niger or A. nidulans. The method enables high quantities
CC of chitin and chitosan to be produced cost effectively. The present
CC sequence represents an Escherichia coli glucosamine-6-phosphate synthase.
CC It was used to transform yeast for use in the method of the invention.
XX SQ Sequence 609 AA;
Query Match 100.0%; Score 3086; DB 8; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.7e-264;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCGIVGAIARDVAEILLEGRLRLEYRGYDSAGLAVVDAGHMTLRRLRGKVMQAQAAE 60
|||||

Db 1 MCGIVGAIQRDVAEILLEGRLRLEYRGYDSAGLAVDAEGHMTLRRLRGKVMQAQAE 60
Qy 61 EHLPLGGTGIATRWATHGEPSEVNAHPVSEHIVVHNGIIEHNEPLRELKARGYTFV 120
Db 61 EHLPLGGTGIATRWATHGEPSEVNAHPVSEHIVVHNGIIEHNEPLRELKARGYTFV 120
Qy 121 SETDTEVIAHLVNWELKGGTLREAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPV 180
Db 121 SETDTEVIAHLVNWELKGGTLREAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPV 180
Qy 181 IGLNGENFIASDQIALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRDIESNLQ 240
Db 181 IGLNGENFIASDQIALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRDIESNLQ 240
Qy 241 YDAGDKGIYRHYMKEIYEQNAIKNTLTGRISHGQVDLSLGNADDELLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMKEIYEQNAIKNTLTGRISHGQVDLSLGNADDELLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRYPFESLAGIPCDVEIASFPRYKSAVRRNSLMTLSQSGETADTLA 360
Db 301 CGTSYNSGMVSRYPFESLAGIPCDVEIASFPRYKSAVRRNSLMTLSQSGETADTLA 360
Qy 361 RLSKELGYLGSIAICNVPGSLVRESDLALMTNAGTEIGVASTKFTTQLTVLLMLVAKL 420
Db 361 RLSKELGYLGSIAICNVPGSLVRESDLALMTNAGTEIGVASTKFTTQLTVLLMLVAKL 420
Qy 421 SRLKGLDASIEHDIVHGLQALPSRIEOMLSQDKRIEALAEFSDKHAFILGRGDQYPIA 480
Db 421 SRLKGLDASIEHDIVHGLQALPSRIEOMLSQDKRIEALAEFSDKHAFILGRGDQYPIA 480
Qy 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDADMPVIVVAPNNLEKLSNIEVRAR 540
Db 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDADMPVIVVAPNNLEKLSNIEVRAR 540
Qy 541 GGQLYVFADQDAGFVSSDNMHIEMPHVEEVIAPFVTVPLQLLAYHVALIKGTVDVQPR 600
Db 541 GGQLYVFADQDAGFVSSDNMHIEMPHVEEVIAPFVTVPLQLLAYHVALIKGTVDVQPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 7
ADW23840

ID ADW23840 standard; protein; 608 AA.

XX AC ADW23840;

XX 07-APR-2005 (first entry)

XX Novel human GPAT protein-related E coli GPAT protein SeqID13.

XX protein purification; glutamine:fructose-6-phosphate amidotransferase;
KW GPAT; antidiabetic; anorectic; metabolic; cyostatic; osteopathic;
KW fungicide; herbicide; diabetes; non-insulin dependent diabetes; obesity;
KW acidosis; cancer; osteoporosis.

XX Escherichia coli.

XX FR2857374-A1.

XX 14-JAN-2005.

XX 08-JUL-2003; 2003FR-00008350.

XX 08-JUL-2003; 2003FR-00008350.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Badet DMAJE, Badet BF;

XX WPI; 2005-076419/09.

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SQ

New modified glutamine:fructose-6-phosphate amidotransferase, useful for identifying specific inhibitors, potentially useful for treating e.g. diabetes, contains a purification tag, also related nucleic acid.

Disclosure; SEQ ID NO 13; 61pp; French.

This invention relates to a novel protein corresponding to human enzymatically active but modified glutamine:fructose-6-phosphate amidotransferase (GPAT). The invention may be useful for the production of compounds with an antidiabetic, anorectic, metabolic, cyostatic, osteopathic, fungicide or herbicide activity. The invention may be used to screen for agents that modify, especially inhibit, its activity, potentially useful as agents for treatment or prevention of diabetes (particularly type II), obesity, acidosis, ketosis, cancer and osteoporosis. In addition inhibitors of plant and fungal GPAT may be useful as herbicides and fungicides, respectively. The present sequence is that of a human GPAT-like protein of the invention.

Sequence 608 AA;

Query Match 99.8%; Score 3081; DB 9; Length 608;

Best Local Similarity 100.0%; Pred. No. 1.3e-263;

Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CGIVGAIQRDVAEILLEGRLRLEYRGYDSAGLAVDAEGHMTLRRLRGKVMQAQAE 61

Db 1 CGIVGAIQRDVAEILLEGRLRLEYRGYDSAGLAVDAEGHMTLRRLRGKVMQAQAE 60

Qy 62 HPLHGGTGIATRWATHGEPSEVNAHPVSEHIVVHNGIIEHNEPLRELKARGYTFVS 121

Db 61 HPLHGGTGIATRWATHGEPSEVNAHPVSEHIVVHNGIIEHNEPLRELKARGYTFVS 120

Qy 122 ETDTEVIAHLVNWELKGGTLREAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPV 181

Db 121 ETDTEVIAHLVNWELKGGTLREAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPV 180

Qy 182 GLNGENFIASDQIALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRDIESNLQ 241

Db 181 GLNGENFIASDQIALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRDIESNLQ 240

Qy 242 DAGDKGIYRHYMKEIYEQNAIKNTLTGRISHGQVDLSLGNADDELLSKVEHIQILA 301

Db 241 DAGDKGIYRHYMKEIYEQNAIKNTLTGRISHGQVDLSLGNADDELLSKVEHIQILA 300

Qy 302 GTSYNSGMVSRYPFESLAGIPCDVEIASFPRYKSAVRRNSLMTLSQSGETADTLA 361

Db 301 GTSYNSGMVSRYPFESLAGIPCDVEIASFPRYKSAVRRNSLMTLSQSGETADTLA 360

Qy 362 LSKELGYLGSIAICNVPGSLVRESDLALMTNAGTEIGVASTKFTTQLTVLLMLVAKL 421

Db 361 LSKELGYLGSIAICNVPGSLVRESDLALMTNAGTEIGVASTKFTTQLTVLLMLVAKL 420

Qy 422 RLKGLDASIEHDIVHGLQALPSRIEOMLSQDKRIEALAEFSDKHAFILGRGDQYPIA 481

Db 421 RLKGLDASIEHDIVHGLQALPSRIEOMLSQDKRIEALAEFSDKHAFILGRGDQYPIA 480

Qy 482 EGALKLKEISYTHAEAYAGELKHGPLALIDADMPVIVVAPNNLEKLSNIEVRAR 541

Db 481 EGALKLKEISYTHAEAYAGELKHGPLALIDADMPVIVVAPNNLEKLSNIEVRAR 540

Qy 542 GQLYVFADQDAGFVSSDNMHIEMPHVEEVIAPFVTVPLQLLAYHVALIKGTVDVQPR 601

Db 541 GQLYVFADQDAGFVSSDNMHIEMPHVEEVIAPFVTVPLQLLAYHVALIKGTVDVQPR 600

Qy 602 LAKSVTVE 609

Db 601 LAKSVTVE 608

RESULT 8

AAYS8827

ID AAYS8827 standard; protein; 609 AA.

CC coli, that includes a modified Glc6P synthase. Production of the
CC glucosamine by recombinant strain 2123-149 (pKLN23-149) was marginally
CC increased when compared to a strain expressing wild-type Glc6P synthase
XX
SQ Sequence 609 AA;

Query Match 99.8%; Score 3080; DB 3; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.6e-263;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIARDVAEILLEGRLRYGYDSAGLAVVDAEGHMTLRRLRGKQVQLAAAE 60
Db 1 MCGIVGAIARDVAEILLEGRLRYGYDSAGLAVVDAEGHMTLRRLRGKQVQLAAAE 60
Qy 61 EPHLHGCGTGAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHPELREELKARGYTFV 120
Db 61 EPHLHGCGTGAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHPELREELKARGYTFV 120
Qy 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Qy 181 IGLGMENFIASDQALLPVTRRPFIELEGDIAEITRRSVNIFDKTGAEVKQDIESNLQ 240
Db 181 IGLGMENFIASDQALLPVTRRPFIELEGDIAEITRRSVNIFDKTGAEVKQDIESNLQ 240
Qy 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSLGPNADELLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSLGPNADELLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASEFRYKSAVRNLSMITLSQSGETADTLA 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASEFRYKSAVRNLSMITLSQSGETADTLA 360
Qy 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQLTVLLMLVAKL 420
Db 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQLTVLLMLVAKL 420
Qy 421 SRLKGLDASTIEHDIVHGLQALPSRIEQMLSODKRIEALAEDFSCKHAFILGRGDQYPTA 480
Db 421 SRLKGLDASTIEHDIVHGLQALPSRIEQMLSODKRIEALAEDFSCKHAFILGRGDQYPTA 480
Qy 481 LEGALKKEISYTHAAYAAGELKHGFLALIDAMPVIVVAPNNELLEKLKNIEVRAR 540
Db 481 LEGALKKEISYTHAAYAAGELKHGFLALIDAMPVIVVAPNNELLEKLKNIEVRAR 540
Qy 541 GGQLYVFADQDAGFVSSDNNHIIEMPHVEEVIAPIFVTVPLQLLAYHVALIKGTDVDQPR 600
Db 541 GGQLYVFADQDAGFVSSDNNHIIEMPHVEEVIAPIFVTVPLQLLAYHVALIKGTDVDQPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 10
AD138865
ID AD138865 standard; protein; 609 AA.
XX
AC AD138865;
XX
DT 15-APR-2004 (first entry)
XX
DE Mutant glucosamine-6-phosphate synthase, SEQ ID 10.
XX
KW Glucosamine; N-acetylglucosamine; fermentation;
KW glucosamine-6-phosphate acetyltransferase;
KW glucosamine-6-phosphate synthase; glucosamine-6-phosphate deaminase;
KW glucosamine-1 phosphate N-acetyltransferase; glucosamine-6-phosphate;
KW glucosamine-1-phosphate; N-acetylglucosamine-1-phosphate;
XX N-acetylglucosamine-6-phosphate; enzyme.
XX Escherichia coli.

Synthetic.
PN WO2004003175-A2.
XX
PD 08-JAN-2004.
PF 01-JUL-2003; 2003WO-US020925.
XX
PR 01-JUL-2002; 2002US-0393348P.
XX
PA (ARKI-) ARKION LIFE SCI LLC.
XX
PI Deng M, Angerer JD, Cyron D, Grund AD, Jerrell TA, Leanna C;
PI Mathre O, Rosson R, Running J, Severson D, Song L, Wassink S;
XX
DR WPI; 2004-203380/19.
DR N-PSDB; ADI38864.
XX
PT Producing glucosamine or N-acetylglucosamine by fermentation involves
PT culturing microorganism comprising glucosamine-6-phosphate
PT acetyltransferase, in fermentation medium, and collecting product.

Claim 15; SEQ ID NO 10; 327pp; English.
XX
PS The present invention relates to a method (M1) for producing glucosamine
CC and N-acetylglucosamine by fermentation. The method comprises (a)
CC culturing in a fermentation medium a microorganism (I) which comprises
CC endogenous glucosamine-6-phosphate acetyltransferase (II) and a genetic
CC modification that increases the activity of (II), glucosamine-6-phosphate
CC synthase (III) or glucosamine-6-phosphate deaminase (IV), or decreases
CC the activity of (IV) and increases the activity of glucosamine-1
CC phosphate N-acetyltransferase (V), and (b) and collecting the product,
CC which is chosen from the group consisting of glucosamine-6-phosphate, N-
CC glucosamine, glucosamine-1-phosphate, N-acetylglucosamine-1-phosphate, N-
CC acetylglucosamine-6-phosphate, and N-acetylglucosamine. The present
CC sequence was used to illustrate the method of the invention.

Sequence 609 AA;

Query Match 99.8%; Score 3080; DB 8; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.6e-263;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIARDVAEILLEGRLRYGYDSAGLAVVDAEGHMTLRRLRGKQVQLAAAE 60
Db 1 MCGIVGAIARDVAEILLEGRLRYGYDSAGLAVVDAEGHMTLRRLRGKQVQLAAAE 60
Qy 61 EPHLHGCGTGAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHPELREELKARGYTFV 120
Db 61 EPHLHGCGTGAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHPELREELKARGYTFV 120
Qy 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Qy 181 IGLGMENFIASDQALLPVTRRPFIELEGDIAEITRRSVNIFDKTGAEVKQDIESNLQ 240
Db 181 IGLGMENFIASDQALLPVTRRPFIELEGDIAEITRRSVNIFDKTGAEVKQDIESNLQ 240
Qy 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSLGPNADELLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSLGPNADELLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASEFRYKSAVRNLSMITLSQSGETADTLA 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASEFRYKSAVRNLSMITLSQSGETADTLA 360
Qy 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQLTVLLMLVAKL 420
Db 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQLTVLLMLVAKL 420
Qy 421 SRLKGLDASTIEHDIVHGLQALPSRIEQMLSODKRIEALAEDFSCKHAFILGRGDQYPTA 480

Db 421 SRLKGLDASIEHDIHVHGLQALPSRIEQLMSQDKRIEALAEFSDKHAFLSRGDQVPIA 480
Qy 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNLEKLSNTEEVRR 540
Db 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNLEKLSNTEEVRR 540
Qy 541 GGQLYVPADQDAGFVSSDNMHIIMPHVEEVIPIFYTVPLQLLAYHVALIKGTVDVQPR 600
Db 541 GGQLYVPADQDAGFVSSDNMHIIMPHVEEVIPIFYTVPLQLLAYHVALIKGTVDVQPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 11
ADI38867
ID ADI38867 standard; protein; 609 AA.
XX AC
XX ADI38867;
DT 15-APR-2004 (first entry)
XX DE
XX DE Mutant glucosamine-6-phosphate synthase, SEQ ID 12.
XX KW Glucosamine; N-acetylglucosamine; fermentation;
KW KW glucosamine-6-phosphate acetyltransferase;
KW KW glucosamine-6-phosphate synthase; glucosamine-6-phosphate deaminase;
KW KW glucosamine-1-phosphate N-acetyltransferase; glucosamine-6-phosphate;
KW KW glucosamine-1-phosphate; N-acetylglucosamine-1-phosphate;
KW KW N-acetylglucosamine-6-phosphate; enzyme.
XX OS Escherichia coli.
OS Synthetic.
XX PN W02004003175-A2.
XX PD
XX PD 08-JAN-2004.
XX PF 01-JUL-2003; 2003WO-US020925.
XX PR 01-JUL-2002; 2002US-0393348P.
XX PA (ARKI-) ARKION LIFE SCI LLC.
XX PI Deng M, Angerer JD, Cyron D, Grund AD, Jerrell TA, Leanna C;
PI Mathre O, Rosson R, Running J, Severson D, Song L, Wassink S;
XX WPI; 2004-203380/19.
DR N-PSDB; ADI38866.
XX PT Producing glucosamine or N-acetylglucosamine by fermentation involves
PT culturing microorganism comprising glucosamine-6-phosphate
PT acetyltransferase, in fermentation medium, and collecting product.
XX PS
PS Claim 15; SEQ ID NO 12; 327pp; English.
XX CC
XX CC The present invention relates to a method (M1) for producing glucosamine
CC and N-acetylglucosamine by fermentation. The method comprises (a)
CC culturing in a fermentation medium a microorganism (I) which comprises
CC endogenous glucosamine-6-phosphate acetyltransferase (II) and a genetic
CC modification that increases the activity of (II), glucosamine-6-phosphate
CC synthase (III) or glucosamine-6-phosphate deaminase (IV), or decreases
CC the activity of (IV) and increases the activity of glucosamine-1
CC phosphate N-acetyltransferase (V), and (b) and collecting the product,
CC which is chosen from the group consisting of glucosamine-6-phosphate,
CC glucosamine, glucosamine-1-phosphate, N-acetylglucosamine-1-phosphate, N-
CC acetylglucosamine-6-phosphate, and N-acetylglucosamine. The present
CC sequence was used to illustrate the method of the invention.
XX SQ
SQ Sequence 609 AA;

Query Match 99.8%; Score 3080; DB 8; Length 609;

Best Local Similarity 99.8%; Pred. No. 1.6e-263;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGTVGAIAORDVAEIILEGRLRLEYRGYDSAGLAVDAEGHMTLRRLRGKVQMLAQAAE 60
Db 1 MCGTVGAIAORDVAEIILEGRLRLEYRGYDSAGLAVDAEGHMTLRRLRGKVQMLAQAAE 60
Qy 61 EHPHGGTGIAHTRWATHGEPSEVNAHPHVSEHIVVHNGIIEHNEPLREELKARGYTFV 120
Db 61 EHPHGGTGIAHTRWATHGEPSEVNAHPHVSEHIVVHNGIIEHNEPLREELKARGYTFV 120
Qy 121 SETDTEVIAHLVNWELKQGGTLREAVLRALPOLRGAYGTVMDSRHPDTLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGTLREAVLRALPOLRGAYGTVMDSRHPDTLAARSGSPLV 180
Qy 181 IGLMGENFIASDQALLPVTRRPFIEEGDIAETRRSVNIPDKTGAEVKRDIESNIQ 240
Db 181 IGLMGENFIASDQALLPVTRRPFIEEGDIAETRRSVNIPDKTGAEVKRDIESNIQ 240
Qy 241 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSSELGNADLLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSSELGNADLLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASBFRYKSAVRNNSMLITLSQGETADTLAGL 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASBFRYKSAVRNNSMLITLSQGETADTLAGL 360
Qy 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFITLTLLMLVAKL 420
Db 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFITLTLLMLVAKL 420
Qy 421 SRLKGLDASIEHDIHVHGLQALPSRIEQLMSQDKRIEALAEFSDKHAFLSRGDQVPIA 480
Db 421 SRLKGLDASIEHDIHVHGLQALPSRIEQLMSQDKRIEALAEFSDKHAFLSRGDQVPIA 480
Qy 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNLEKLSNTEEVRR 540
Db 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNLEKLSNTEEVRR 540
Qy 541 GGQLYVPADQDAGFVSSDNMHIIMPHVEEVIPIFYTVPLQLLAYHVALIKGTVDVQPR 600
Db 541 GGQLYVPADQDAGFVSSDNMHIIMPHVEEVIPIFYTVPLQLLAYHVALIKGTVDVQPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 12
AAVS8825
ID AAVS8825 standard; protein; 609 AA.
XX AC AAVS8825;
XX DT 08-MAY-2000 (first entry)
XX DE
XX DE E. coli glucosamine-6-phosphate synthase mutant GlcN6P-S-124.
XX KW Glucosamine-6-phosphate synthase; glms gene; mutant; GlcN6P-S-124;
KW KW glucosamine; metabolic engineering; plasmid pKLN23-124; mutcin.
XX OS Escherichia coli.
XX PH Key Location/Qualifiers
FT Misc-difference 469 /note= "replaces wild-type Leu"
XX FT
XX PN W0200004182-A1.
XX XX
XX PD 27-JAN-2000.
XX PF 15-JUL-1999; 99WO-US015976.
XX XX

PR 15-JUL-1998; 98US-00115475.
XX (DCVB-) DCV INC DBA BIO-TECH RESOURCES.
XX Berry A, Burlingame RP, Millis JR;
PI WPI; 2000-182441/16.
DR N-PSDB; AAZ58252.
XX
XX Fermentation of E. coli having an altered amino acid sugar metabolic
PT pathway to produce glucosamine, especially using novel recombinant
PT variant glucosamine-6-phosphate synthases.
XX
PS Claim 28; Page 130-132; 150pp; English.
XX
CC The present sequence is that of a mutant, denoted GlcN6P-S-124, of the
CC glucosamine-6-phosphate synthase (GlcN6P synthase) of Escherichia coli.
CC When compared with the wild-type sequence (see AAY58822), the mutant
CC includes a Leu-469 to Thr amino acid substitution. This alteration is
CC predicted from the mutated glms gene in plasmid pKLN23-124 (see AAZ58252).
CC The invention provides methods for the overproduction of glucosamine by
CC fermentation using a genetically engineered microorganism, especially E.
CC coli, that includes a modified GlcN6P synthase. Production of the
CC glucosamine by recombinant strain 2123-124 (pKLN23-124) was significantly
CC increased when compared to a strain expressing wild-type Glc6NP synthase
CC owing to reduced product inhibition
XX
SQ Sequence 609 AA;

Query Match 99.8%; Score 3079; DB 3; Length 609;
Best Local Similarity 99.8%; Pred. No. 2e-263;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIAQDVAEILLEGRLRYGYDSAGLAVDAEGHMTLRLRLKGVQMLAQAAE 60
Db 1 MCGIVGAIAQDVAEILLEGRLRYGYDSAGLAVDAEGHMTLRLRLKGVQMLAQAAE 60
Qy 61 EPHLHGCTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIENHPELREELKARGYTFV 120
Db 61 EPHLHGCTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIENHPELREELKARGYTFV 120
Qy 121 SETDTEVIAHLVNWELKQGTLEAVLRAIPQLRGAYGVIMDSRHPDTLLAARSGSPVLV 180
Db 121 SETDTEVIAHLVNWELKQGTLEAVLRAIPQLRGAYGVIMDSRHPDTLLAARSGSPVLV 180
Qy 181 IGLGMGNFTASDQALLPVTRRFIFLEEGDIAEITRRSVNIPDKTGAEVKQDIESNLQ 240
Db 181 IGLGMGNFTASDQALLPVTRRFIFLEEGDIAEITRRSVNIPDKTGAEVKQDIESNLQ 240
Qy 241 YDAGDKGIYRHYMQEIQPNAIKNTLTGRISHGQVDLSLGPNADELLSKVHIQILA 300
Db 241 YDAGDKGIYRHYMQEIQPNAIKNTLTGRISHGQVDLSLGPNADELLSKVHIQILA 300
Qy 301 CGTSYNSGMVSRVWFSLSAGIPCDVEIASFEFRYKSAVRNSLMTLSQSGTADTLA 360
Db 301 CGTSYNSGMVSRVWFSLSAGIPCDVEIASFEFRYKSAVRNSLMTLSQSGTADTLA 360
Qy 361 RLSKELGYLSLAICNVPSSLVRESDLALMTNAGTEIGVASTKFTTTLVLMVAKL 420
Db 361 RLSKELGYLSLAICNVPSSLVRESDLALMTNAGTEIGVASTKFTTTLVLMVAKL 420
Qy 421 SRLKGLDASIEHDIHGLQALPSRIEQMLSQDKRIEALAEFSDKHAFLLGRGQYPIA 480
Db 421 SRLKGLDASIEHDIHGLQALPSRIEQMLSQDKRIEALAEFSDKHAFLLGRGQYPIA 480
Qy 481 LEGALKKEISYTHAAYAGELKHGFLALIDAMPVIVVAPNNELKELKSNIEVRAR 540
Db 481 LEGALKKEISYTHAAYAGELKHGFLALIDAMPVIVVAPNNELKELKSNIEVRAR 540
Qy 541 GGQLYVFAQDQAGFVSSDNNHIIEMPHVEVIAPIFYTVPLQLLAYHVALIKGTDVDDQR 600
Db 541 GGQLYVFAQDQAGFVSSDNNHIIEMPHVEVIAPIFYTVPLQLLAYHVALIKGTDVDDQR 600

Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609
RESULT 13
ADI38863
ID ADI38863 standard; protein; 609 AA.
XX
XX ADI38863;
AC
XX 15-APR-2004 (first entry)
DT
XX
DE Mutant glucosamine-6-phosphate synthase, glms*124, SEQ ID 8.
XX
XX Glucosamine; N-acetylglucosamine; fermentation;
KW glucosamine-6-phosphate acetyltransferase;
KW glucosamine-6-phosphate synthase; glucosamine-6-phosphate deaminase;
KW glucosamine-1 phosphate N-acetyltransferase; glucosamine-6-phosphate;
KW glucosamine-1-phosphate; N-acetylglucosamine-1-phosphate;
KW N-acetylglucosamine-6-phosphate; enzyme.
XX
XX Escherichia coli.
OS
OS Synthetic.
PN WO2004003175-A2.
XX
XX 08-JAN-2004.
PD
XX
XX 01-JUL-2003; 2003WO-US020925.
PF
XX
XX 01-JUL-2002; 2002US-0393348P.
PR
XX
XX (ARKI-) ARKION LIFE SCI LLC.
PA
XX
XX Deng M, Angerer JD, Cyron D, Grund AD, Jerrell TA, Leanna C;
PI Mathre O, Rosson R, Running J, Severson D, Song L, Wassink S;
PI
XX
XX WPI; 2004-203380/19.
DR
XX
XX N-PSDB; ADI38862.
DR
XX
XX Producing glucosamine or N-acetylglucosamine by fermentation involves
PT culturing microorganism comprising glucosamine-6-phosphate
PT acetyltransferase, in fermentation medium, and collecting product.
XX
XX
PS Claim 15; SEQ ID NO 8; 327pp; English.
XX
XX The present invention relates to a method (M1) for producing glucosamine
CC and N-acetylglucosamine by fermentation. The method comprises (a)
CC culturing in a fermentation medium a microorganism (I) which comprises
CC endogenous glucosamine-6-phosphate acetyltransferase (II) and a genetic
CC modification that increases the activity of (II), glucosamine-6-phosphate
CC synthase (III) or glucosamine-6-phosphate deaminase (IV), or decreases
CC the activity of (IV) and increases the activity of glucosamine-1
CC phosphate N-acetyltransferase (V), and (b) and collecting the product,
CC which is chosen from the group consisting of glucosamine-6-phosphate,
CC glucosamine, glucosamine-1-phosphate, N-acetylglucosamine-1-phosphate,
CC acetylglucosamine-6-phosphate, and N-acetylglucosamine. The present
CC sequence was used to illustrate the method of the invention.
XX
SQ Sequence 609 AA;

Query Match 99.8%; Score 3079; DB 8; Length 609;
Best Local Similarity 99.8%; Pred. No. 2e-263;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIAQDVAEILLEGRLRYGYDSAGLAVDAEGHMTLRLRLKGVQMLAQAAE 60
Db 1 MCGIVGAIAQDVAEILLEGRLRYGYDSAGLAVDAEGHMTLRLRLKGVQMLAQAAE 60
Qy 61 EPHLHGCTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIENHPELREELKARGYTFV 120
Db 61 EPHLHGCTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIENHPELREELKARGYTFV 120

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 7, 2006, 09:25:03 ; Search time 25 Seconds
(without alignments)
2343.840 Million cell updates/sec

Title: US-10-612-779-2

Perfect score: 3086

Sequence: 1 MCGIVGAIQAQRDVAEILLEG.....LIKGTDVDOPRNLAKSVTVE 609

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: piri.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3086	100.0	609	1	XNECGM	glutamine-fructose
2	3082	99.9	609	2	H86058	hypothetical prote
3	3075	99.6	609	2	G91212	hypothetical prote
4	3053	98.9	609	2	AB0955	glutamine-fructose
5	2682	86.9	609	2	AB0500	glutamine-fructose
6	2270.5	73.6	610	2	D64067	glutamine-fructose
7	2264.5	73.4	610	2	F82316	glutamine-fructose
8	1995	64.6	611	2	F82351	glutamine-fructose
9	1868	60.5	621	2	A84933	glutamine-fructose
10	1702	55.2	635	2	E71272	glutamine-fructose
11	1695	54.9	609	2	A82844	glutamine-fructose
12	1597	51.7	611	2	T45493	glutamine-fructose
13	1570.5	50.9	612	2	H82022	glutamine-fructose
14	1566.5	50.8	612	2	B81246	glutamine-fructose
15	1449	47.0	612	2	AD3595	glutamine-fructose
16	1435.5	46.5	608	2	B95322	NodM Glutamine ami
17	1427.5	46.3	608	2	C97575	glutamine-fructose
18	1427.5	46.3	608	2	AC2796	hypothetical prote
19	1411.5	45.7	604	2	C69793	glutamine-fructose
20	1371.5	44.4	606	2	A75336	glutamine-fructose
21	1361.5	44.1	592	2	D70327	glutamine-fructose
22	1340.5	43.4	608	1	S01040	glutamine-fructose
23	1339	43.4	605	2	S16561	glutamine-fructose
24	1337.5	43.3	606	2	B87263	hypothetical prote
25	1327.5	43.0	598	2	F75212	glutamine-fructose
26	1314.5	42.6	606	2	B72412	glutamine-fructose
27	1297.5	42.0	608	2	C96919	glutamine-fructose
28	1293	41.9	615	2	T35569	glutamine-fructose
29	1292.5	41.9	601	2	D71248	glutamine-fructose

RESULT 1

XNECGM

glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - Escherichia coli
N;Alternate names: glucosamine-6-phosphate synthase; glucosaminophosphate isomerase (gluc
e
C;Species: Escherichia coli
C;Date: 31-Mar-1990 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
R;Accession: B65176; A30389; I41219; S17839; Q90513
R;Plattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B65176
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-609 <BLAT>
A;Cross-references: UNIPROT:P17169; UNIPARC:UPI0000157CA3; GB:AE000450; GB:U00096; NID:g
A;Experimental source: strain K-12, substrain MG1655
R;Walker, J.E.; Gay, N.J.; Saraste, M.; Eberle, A.N.
Biochem. J. 224, 799-815, 1984
A;Title: DNA sequence around the Escherichia coli unc operon. Completion of the sequence
A;Reference number: A30389; MUID:85121806; PMID:6395859
A;Accession: A30389
A;Molecule type: DNA
A;Residues: 1-418,'NV',421-609 <WAL>
A;Cross-references: UNIPARC:UPI000016F5F4; GB:X01631; NID:g43256; PIDN:CAA25785.1; PID:g
R;McKown, R.L.; Orle, K.A.; Chen, T.; Craig, N.L.
J. Bacteriol. 170, 352-358, 1988
A;Title: Sequence requirements of Escherichia coli attTn7, a specific site of transposon
A;Reference number: I41219; MUID:88086894; PMID:2826397
A;Accession: I41219
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 597-609 <RES>
A;Cross-references: UNIPARC:UPI000016F18D; GB:M18980; NID:g146074; PIDN:AAA23836.1; PID:g
R;Gollinelli-Pimpaneau, B.; Badet, B.
Eur. J. Biochem. 201, 175-182, 1991
A;Title: Possible involvement of Lys603 from Escherichia coli glucosamine-6-phosphate syr
A;Reference number: S17839; MUID:92007872; PMID:1915361
A;Accession: S17839
A;Molecule type: protein
A;Residues: 49-50,'X',52-53;218;219;220-223,'X',225-231;489-493;504-508;'K';'K';601-609-
4A7
A;Cross-references: UNIPARC:UPI000011EBBE; UNIPARC:UPI000011ECBE; UNIPARC:UPI000011ECBE;
C;Genetics:
A;Gene: glms
A;Map position: 4 min
C;Function:
A;Description: catalyzes the formation of D-glucosamine-6-phosphate from the amido group
A;Pathway: Glucosamine biosynthesis
A;Note: Glucosamine-6-phosphate is used in the biosynthesis of amino sugars of asparagine

ALIGNMENTS

C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C;Keywords: aminotransferase; isomerase
F;2-609/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predicted
F;2/Active site: Cys #status predicted

Query Match 100.0%; Score 3086; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 2e-191;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCGIVGAIAQRDVAEILLEGRLRLEVRGYDSAGLAVVDAEGHMTLRRLRGKVKQMLAAQAAE 60
Db 1 MCGIVGAIAQRDVAEILLEGRLRLEVRGYDSAGLAVVDAEGHMTLRRLRGKVKQMLAAQAAE 60
Qy 61 EHPHGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHHPRLREELKARGYTFV 120
Db 61 EHPHGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHHPRLREELKARGYTFV 120
Qy 121 SETDTEVIAHLVNWELKQGGLTREAIVRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGLTREAIVRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Qy 181 IGLGMENFTASQDALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKQDIESNLQ 240
Db 181 IGLGMENFTASQDALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKQDIESNLQ 240
Qy 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADELLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADELLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASSEFRYKSAVRNSLMITLSQSGETADTLAGL 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASSEFRYKSAVRNSLMITLSQSGETADTLAGL 360
Qy 361 RLSKELGYLGS LAICNVPGSSLVRESDLALMTNAGTEIGVASTKATFTQLTVLLMLVAKL 420
Db 361 RLSKELGYLGS LAICNVPGSSLVRESDLALMTNAGTEIGVASTKATFTQLTVLLMLVAKL 420
Qy 421 SRLKGLDASIEHDI VHGLQALPSRIEQMLSDQRIEALAEFSDKHAFFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDI VHGLQALPSRIEQMLSDQRIEALAEFSDKHAFFLGRGDQYPIA 480
Qy 481 LEGALKKEISYTHAEAYAAGELKHGFLALIDAMPVIVVAPNNELLEKLSNIEVRAR 540
Db 481 LEGALKKEISYTHAEAYAAGELKHGFLALIDAMPVIVVAPNNELLEKLSNIEVRAR 540
Qy 541 GGQLYVFADQDAGFVSSDNMHIIEMPHVEEVIAPFYFTVPLQLLAYHVALIKGTVDVQPR 600
Db 541 GGQLYVFADQDAGFVSSDNMHIIEMPHVEEVIAPFYFTVPLQLLAYHVALIKGTVDVQPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 2
H86058
hypothetical protein glms [imported] - Escherichia coli (strain O157:H7, substrain EDL93)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H86058
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: H86058
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-609 <STO>
A;Cross-references: UNIPROT:Q8XEG2; UNIPARC:UPI0000165991; GB:AE005174; NID:g12518593; F
C;Genetics:
A;Gene: glms

C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C;Keywords: aminotransferase; isomerase
F;2-609/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predicted
F;2/Active site: Cys #status predicted

Query Match 99.9%; Score 3082; DB 2; Length 609;
Best Local Similarity 99.8%; Pred. No. 3.7e-191;
Matches 608; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCGIVGAIAQRDVAEILLEGRLRLEVRGYDSAGLAVVDAEGHMTLRRLRGKVKQMLAAQAAE 60
Db 1 MCGIVGAIAQRDVAEILLEGRLRLEVRGYDSAGLAVVDAEGHMTLRRLRGKVKQMLAAQAAE 60
Qy 61 EHPHGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHHPRLREELKARGYTFV 120
Db 61 EHPHGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHHPRLREELKARGYTFV 120
Qy 121 SETDTEVIAHLVNWELKQGGLTREAIVRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGLTREAIVRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Qy 181 IGLGMENFTASQDALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKQDIESNLQ 240
Db 181 IGLGMENFTASQDALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKQDIESNLQ 240
Qy 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADELLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADELLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASSEFRYKSAVRNSLMITLSQSGETADTLAGL 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASSEFRYKSAVRNSLMITLSQSGETADTLAGL 360
Qy 361 RLSKELGYLGS LAICNVPGSSLVRESDLALMTNAGTEIGVASTKATFTQLTVLLMLVAKL 420
Db 361 RLSKELGYLGS LAICNVPGSSLVRESDLALMTNAGTEIGVASTKATFTQLTVLLMLVAKL 420
Qy 421 SRLKGLDASIEHDI VHGLQALPSRIEQMLSDQRIEALAEFSDKHAFFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDI VHGLQALPSRIEQMLSDQRIEALAEFSDKHAFFLGRGDQYPIA 480
Qy 481 LEGALKKEISYTHAEAYAAGELKHGFLALIDAMPVIVVAPNNELLEKLSNIEVRAR 540
Db 481 LEGALKKEISYTHAEAYAAGELKHGFLALIDAMPVIVVAPNNELLEKLSNIEVRAR 540
Qy 541 GGQLYVFADQDAGFVSSDNMHIIEMPHVEEVIAPFYFTVPLQLLAYHVALIKGTVDVQPR 600
Db 541 GGQLYVFADQDAGFVSSDNMHIIEMPHVEEVIAPFYFTVPLQLLAYHVALIKGTVDVQPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 3
G91212
hypothetical protein Ecs4671 [imported] - Escherichia coli (strain O157:H7, substrain R11
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: G91212
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: G91212
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-609 <HAY>
A;Cross-references: UNIPROT:Q8XEG2; UNIPARC:UPI000016552F; GB:BA000007; PIDN:BAE38094.1;
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: Ecs4671
C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
Query Match 99.6%; Score 3075; DB 2; Length 609;

[illegible]

RESULT 4
AB0955
glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - Salmonella ent
N:Alternate names: Glucosamine-fructose-6-P aminotransferase [misnomer]
C:Species: Salmonella enterica subsp. enterica serovar Typhi
C:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 28-Jul-2003
C:Accession: AB0955
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AB0955
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-609 <PAR>
A:Cross-references: UNIPARC:UPI000005A683; GB:AL513382; PIDN:CAD03134.1; PID:g16504770;
C:Genetics:
A:Gene: STY3917
C:Superfamily: Glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C:Keywords: aminotransferase; isomerase

Query Match	98.9%;	Score 3053;	DB 2;	Length 609;
Best Local Similarity	98.5%;	Pred. No. 2.7e-189;		
Matches 600;	Conservative 5;	Mismatches 4;	Indels 0;	Gaps 0;
Qy	1	MCGIVGAIAQRDVAEILLEGRLRLRYGYSAGLAVVDAEGHMTLRRLRGKVQMLAQAAE	60	
Db	1	MCGIVGAIAQRDVAEILLEGRLRLRYGYSAGLAVVDAEGHMTLRRLRGKVQMLAQAAE	60	
Qy	61	EHPHUGGTGIAHTRWATHGPPSEVNAHPHVSSEHIVVPHNGIIENHPELREELKARGTTFV	120	
Db	61	EHPHUGGTGIAHTRWATHGPPSEANAPHVSEHIVVPHNGIIENHPELREALKARGTTFV	120	
Qy	121	SETDTEVIAHLVNWELKQGGTLREAVLURAIPLQLRGAYGTVMDSRHPDPTLLAARSGSPLV	180	
Db	121	SETDTEVIAHLVNWELKQGGTLRDAIURAIPLQLRGAYGTVMDSRHPDPTLLAARSGSPLV	180	
Qy	181	IGLGMGNFIASDQLALLPVTRRPFIFLEEGDIAEITRRSVNIFDKTGAEVKRRQDIESNLQ	240	
Db	181	IGLGMGNFIASDQLALLPVTRRPFIFLEEGDIAEITRRSVNIFDNTGAEVKRRQDIESNLQ	240	
Qy	241	YDAGDKGIRYHYWQKEIYEOPNAIKNTLTGRI SHGQVDLSLSELGNADLLSKVHEHIOILA	300	
Db	241	YDAGDKGIRYHYWQKEIYEOPNAIKNTLTGRI SHGQVDLSLSELGNADLLSKVHEHIOILA	300	
Qy	301	CGTSYNSGMVSRVWFESLAGIPCDVEIASFRRYKSAVRNSLMI TLSQSETADTTLAGL	360	
Db	301	CGTSYNSGMVSRVWFESLAGIPCDVEIASFRRYKSAVRNSLMI TLSQSETADTTLAGL	360	
Qy	361	RLSKELGYLGS LAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTOLTVLMLVAKL	420	
Db	361	RLSKELGYLGS LAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTOLTVLMLVAKL	420	
Qy	421	SRUKGLDASIEHDI VHGLQALPSRIEQMLSQDKRI IEALAE DFD SKHHAL FLGRGDQVPIA	480	
Db	421	SRUKGLDASIEHDI VHGLQALPSRIEQMLSQDKRI ELAE DFD SKHHAL FLGRGDQVPIA	480	
Qy	481	LEGALKLUKEI SYTHAEAYAAGELKHGPLALIDADMPVIVVAPNNELLEKLKSNTEEVRRAR	540	
Db	481	LEGALKLUKEI SYTHAEAYAAGELKHGPLALIDADMPVIVVAPNNELLEKLKSNTEEVRRAR	540	
Qy	541	GGQLYVFADQDAGFVSSDNMHI TEMPHVEEVIAP I FVTVPLQLLAYHVALLI KGTDVDQPR	600	
Db	541	GGQLYVFADQDAGFVSSDNMHI TEMPHVEEVIAP I FVTVPLQLLAYHVALLI KGTDVDQPR	600	
Qy	601	NLAKSVTVE	609	
Db	601	NLAKSVTVE	609	

RESULT 5

AB0500
glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) [imported] - Yer

C:Species: *Yersinia pestis*

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C:Accession: AB0500

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001

A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.

A:Reference number: AB0001; PMID:21470413; PMID:11586360

A:Accession: AB0500

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-609 <KUR>

A:Cross-references: UNIPROT:Q8Z9S8; UNIPARC:UPI0000165B7A; GB:AL590842; PIDN:CAC93567.1;

C:Genetics:

A:Gene: glms

C:Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)

C:Keywords: aminotransferase; isomerase

Query Match 86.9%; Score 2682; DB 2; Length 609;

Best Local Similarity 85.1%; Pred. No. 2.4e-165;

Matches 518; Conservative 44; Mismatches 47; Indels 0; Gaps 0;	
QY 1	1 MCGIVGAIQORDVAEILLEGRLRLEYRGYDSAGLAVDVAEGHMTLRRLGKQVOMLAQAAE 60
Db	1 MCGIVGAIQORDVAEILLEGRLRLEYRGYDSAGLAVDVAEGHMTLRRLGKQVOMLAQAAE 60
QY 61	61 EHPHGGTGTIAHTRWATHGEPSEVNAHPHVSEHIVVHNGIIEENHEPLREELKARGYTFV 120
Db	61 KQDLHGGTGTIAHTRWATHGEPSEANHPHVSDIYSVHNGIIEENHEPLRELLISRGYRFS 120
QY 121	121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPOLRGAYGTVMDSRHPDPTLLAARSGSPLV 180
Db	121 SETDTEVIAHLVHWEQQQSLLELVKRVIPQLRGAYGTVMDSRPSRLTAAARSGSPLV 180
QY 181	181 IGLGNGENFIASDQALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRODIESNLQ 240
Db	181 ICGVGENFIASDQALLPVTRRFIFLEEGDVVEVTRRSISIFDKQGNALIERPEIESQVQ 240
QY 241	241 YDAGDKGIYRHYMQEIIYEQPNAIKNTLTGRISHGOVDLSLGPNADELLSKVEHIQILA 300
Db	241 YDAGDKGIYRHYMQEIIYEQPNAIKNTLEGRLSHGMDLSLGPKADALLAEVQHIQILA 300
QY 301	301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFRYRKSAVRNLSMLITLSQSGETADTLA 360
Db	301 CGTSYNSGMVSRVWFESLAGVPCDVEIASFRYRKSAVRNLSMLITLSQSGETADTLAAL 360
QY 361	361 RLSKELGYLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLVLLMLVAKL 420
Db	361 RLSKELGYLSLAICNVAGSSLVRESDLALMTNAGTEIGVASTKFTTQTLVLLMLVGRK 420
QY 421	421 SRLKGLDASIEHDIVHGLQALPSRIEOMLSODKRIEALAEFSDKHHALFLGRGDQYPI 480
Db	421 GKLKGADASLEHDIVHALQALPARIEOMLSLDKTIEALAEFGSDKHHALFLGRGDQYPIA 480
QY 481	481 LEGALKLKEISYTHAEYAAAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
Db	481 MEGALKLKEISYTHAEYAAAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
QY 541	541 GGQLYVFADQADGAFVSSDNNHIIEMPHVEVIAPIFYTPVPLQALLAYHVALIKGTDVQDP 600
Db	541 GGLLYVFADQADGTFDSEGMKIIQLPHVEIIAPIFYTPVPLQLLSYHVALIKGTDVQDP 600
QY 601	601 NLAQSVTVE 609
Db	601 NLAQSVTVE 609
RESULT 6	
D64067	
glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - Haemophilus influenzae	
C:Species: Haemophilus influenzae	
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004	
C:Accession: D64067	
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995	
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.	
A:Reference number: A64000, MUID:95350630, PMID:7542800	
A:Accession: D64067	
A:Status: nucleic acid sequence not shown; translation not shown	
A:Molecule type: DNA	
A:Residues: 1-610 <TIGR>	
A:Cross-references: UNIPROT:P44708; UNIPARC:UPI00000512BF; GB:U32726; GB:L42023; NID:g19	
A:Note: named as homolog to a protein from Escherichia coli	
C:Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)	
C:Keywords: aminotransferase; isomerase	
F;2-610/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predicted	
F;2/Active site: Cys #status predicted	
Query Match 73.6%; Score 2270.5; DB 2; Length 610;	
Best Local Similarity 72.3%; Pred. No. 8.9e-139;	

Matches 441; Conservative 73; Mismatches 95; Indels 1; Gaps 1;	
QY 1	1 MCGIVGAIQORDVAEILLEGRLRLEYRGYDSAGLAVDVAEGHMTLRRLGKQVOMLAQAAE 60
Db	1 MCGIVGAVAQORDVAEILLEGRLRLEYRGYDSAGVAVINKQNELQIRCLGKVKALDEAVS 60
QY 61	61 EHPHGGTGTIAHTRWATHGEPSEVNAHPHVSEHIVVHNGIIEENHEPLREELKARGYTFV 120
Db	61 EXPLGGTGTIAHTRWATHGEPSETNAHPHSSGTFVAVHNGIIEENHEPLREELKARGYTFV 120
QY 121	121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPOLRGAYGTVMDSRHPDPTLLAARSGSPLV 180
Db	121 SQTDTTEVIAHLVEMWRITDLSLDAVKAVKQLTGAYGNVWDSRHPHLVAARSGSPLV 180
QY 181	181 IGLGNGENFIASDQALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRODIESNLQ 240
Db	181 IGLGIGENFLASDQALLSVTRRFIFLEEGDIAETTRRTVDIYDTHGNKAKREIHESNLE 240
QY 241	241 YDAGDKGIYRHYMQEIIYEQPNAIKNTLTGRISHGOVDLSLGPNADELLSKVEHIQILA 300
Db	241 NDAEKGKFRHFMQKEIYEQPTALINTMEGRINHENVIVDSIGNGAKGILEKVEHIQIVA 300
QY 301	301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFRYRKSAVRNLSMLITLSQSGETADTLA 360
Db	301 CGTSYNAGVARYWFESLAGVSCDVEIASFRYRKFTVRPNLSLLITLSQSGETADTLAAL 360
QY 361	361 RLSKELGYLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLVLLMLVAKL 420
Db	361 RLAKKGYMAALTICNVAGSSLVRESDLAFNTRAGVEVGVAFTKFTTQLAALLMLVATL 420
QY 421	421 SRLKG-LDASIEHDIVHGLQALPSRIEOMLSODKRIEALAEFSDKHHALFLGRGDQYPI 479
Db	421 GKVKGHISVEKEREIIKAWQSLPAIEKALAFDTEIEALAEADPAEKHALFLGRGAFPI 480
QY 480	480 ALEGALKLKEISYTHAEYAAAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEEVR 539
Db	481 AVEASLKLKEISYTHAEYAAAGELKHGPLALIDAMPVIVVAPNNELLEKVKSNIEEVR 540
QY 540	540 RGGQLYVFADQADGAFVSSDNNHIIEMPHVEVIAPIFYTPVPLQALLAYHVALIKGTDVQDP 599
Db	541 RGGQLYVFADKAEAGFTFSEGMKIITMPKVNIDVAPIFYTPVPMQLSYVALIKGTDVQDP 600
QY 600	600 RNLAKSVTVE 609
Db	601 RNLAKSVTVE 610
RESULT 7	
E82316	
glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) [similarity] - Vibrio cholerae	
C:Species: Vibrio cholerae	
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004	
C:Accession: E82316	
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Church, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000	
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.	
A:Reference number: A82035; MUID:20406833; PMID:10952301	
A:Accession: E82316	
A:Status: preliminary	
A:Molecule type: DNA	
A:Residues: 1-610 <NEI>	
A:Cross-references: UNIPROT:Q9KUM8; UNIPARC:UPI0000164853; GB:AE004135; GB:AE003852; NID:	
A:Experimental source: serogroup O1; strain N16961; biotype El Tor	
C:Genetics:	
A:Map position: 1	
A:Gene: VC0487	
C:Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)	
C:Keywords: aminotransferase; isomerase	
F;2-610/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predicted	
F;2/Active site: Cys #status predicted	

Query Match 73.4%; Score 2264.5; DB 2; Length 610;
Best Local Similarity 71.6%; Pred. No. 2.2e-138;
Matches 437; Conservative 72; Mismatches 100; Indels 1; Gaps 1;

Qy 1 MCGIVGIAQORDVAEILLEGRLREYRGYSAGLAVVDAEGHMTLRRLKGVQMLAAAE 60
Db 1 MCGIVGIAQORDVAEILVQGLRLREYRGYSAGVAVVDSKQLTRLRLKGVQELADAVE 60

Qy 61 EHPHGGTGTAHTRWATHGEPSEVNAHPVSHIIVVHNGIIEHPELREELKARGYTFV 120
Db 61 AAQVAGGTGAHTRWATHGEPSEINAPHISGDIIVVHNGIIEHPELRLTMDQGVYFT 120

Qy 121 SETDTEVIAHLVNWELKOGGTLREAVLRAIPQLRGAYGTVMDSRHPDPTLLAARSGPLV 180
Db 121 SQTDTTEVIAHLVNEWELRASLLEAVQTKVQLTGAYGTVMDSRHPDPTLLAARSGSPIV 180

Qy 181 IGLGMENFTASDQALLPVTFRFIFLEEGDIAETIRSVNIYFDKTCAGVKRODIESNLQ 240
Db 181 IGFIGENFTASDQALLNTRFPMYLEEGDVAEMTRDRVRVFDALGQPVOREISESNLE 240

Qy 241 YDAGDKGIYRHYMKEIYEQPNAIKNTLTGRISHGQVDSLSELGPNADLLSKVHEIQILA 300
Db 241 HDADKGRHYRHYMKEIFEQPKALINTMEGRITHDCVVVESIGVHAAEILAKVHVQIVA 300

Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNLSMITLSQSGETADTLAAGL 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNLSMITLSQSGETADTLAAL 360

Qy 361 RLKELGYLGSLAICNVPGSSLVRESDLMTWAGTEIGVASTKAFPTTQLTVLLMLVAKL 420
Db 361 RLAKKGYMAAMTICNVAGSSLVRESDFAPMTRAGTEIGVASTKAFPTTQLTVLLMLVTAL 420

Qy 421 SRL-KGLDASIEHDIHVGLQALPSRIEOMLSODKRIEALAEFSDKHHLFLGRGDQYPI 479
Db 421 GKQOIRIGRELEAEIVHALHQLPKQIETALSFEKQIETLAEDFADKHHTLFLGRGEYPI 480

Qy 480 ALEGALKKEISYTHAEAYAGELKHGPLALIDADMPIVIVVAPNNELLEKLKSNIEVRA 539
Db 481 AVEASLKLKEISYTHAEAYAGELKHGPLALIDADMPIVIVVAPNNELLEKLKSNIEVRA 540

Qy 540 RGQLYVFADQDAGFVSSDNMHIEMPHVEEVIAPITVPLQLLAYHVALIKGTVDQDP 599
Db 541 RGQLYVFADQDAGFVSSDNMHIEMPHVEEVIAPITVPLQLLAYHVALIKGTVDQDP 600

Qy 600 RNLAKSVTVE 609
Db 601 RNLAKSVTVE 610

RESULT 8
F82951
Glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) [similarity] - F
N;Alternate names: aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Species: Pseudomonas aeruginosa
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F82951
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-611 <STO>
A;Cross-references: UNIPROT:Q9HT25; UNIPARC:UPI0000165E0; GB:AE004091; NID
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: glmS; PA5549
C;Superfamily: Glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C;Keywords: aminotransferase; isomerase
F;2-611/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predi
F;2/Active site: Cys #status predicted

Query Match 64.6%; Score 1995; DB 2; Length 611;
Best Local Similarity 62.7%; Pred. No. 5.4e-121;
Matches 383; Conservative 101; Mismatches 125; Indels 2; Gaps 2;

Qy 1 MCGIVGIAQORDVAEILLEGRLREYRGYSAGLAVVDAEGHMTLRRLKGVQMLAAAE 60
Db 1 MCGIVGIAERNTPTILIEGLKREYRGYSAGVAVPDNEGRLQRCRVRGVKASLEEGLA 60

Qy 61 EHPHGGTGTAHTRWATHGEPSEVNAHPVSHIIVVHNGIIEHPELREELKARGYTFV 119
Db 61 GTPLRLGLAHTRWATHGAPTEGNAPHPSSDEAVVHNGIIEHPELRLKGLGYVP 120

Qy 120 VSETDTEVIAHLVNWELKOGGTLREAVLRAIPQLRGAYGTVMDSRHPDPTLLAARSGPL 179
Db 121 TSQTDTEVIVHLLHKLQSIGDLTLAKDAVKELHGLAVLSAAQDRIVAAARSGSPL 180

Qy 180 VIGLGMENFTASDQALLPVTFRFIFLEEGDIAETIRSVNIYFDKTCAGVKRODIESNL 239
Db 181 VIGLGMENFTASDQALLRQVTRFIFLEEGDIAETIRSDVRLWDVQGVQRETQYHE 240

Qy 240 QYDAGDKGIYRHYMKEIYEQPNAIKNTLTGRISHGQVDSLSELGPNADLLSKVHEIQIL 299
Db 241 GABAADKGRHYRHYMKEIHEQPSVORTLEGRIGQVQLVESFGPQAELFAKVRNVQIV 300

Qy 300 ACCTSNGMVSRYWFESLAGIPCDVEIASFPRYKSAVRNLSMITLSQSGETADTLAAG 359
Db 301 ACCTSNGMVSRYWFESLAGIPCDVEIASFPRYKSAVRNLSMITLSQSGETADTLAA 360

Qy 360 LRUSKELGYLGSLAICNVPGSSLVRESDLMTWAGTEIGVASTKAFPTTQLTVLLMLVAK 419
Db 361 LRNAKELGFLSSVAINCVATSSLVRESDLTLLTQAGPEIGVASTKAFPTTQLTVALLTLG 420

Qy 420 LSR-L-KGLDASIEHDIHVGLQALPSRIEOMLSODKRIEALAEFSDKHHLFLGRGDQY 478
Db 421 IGVQKRLADGVAEILVDELRRLPTRLGEALANRTVERKSELFAEKHHTLFLGRGAQFP 480

Qy 479 IALEGALKKEISYTHAEAYAGELKHGPLALIDADMPIVIVVAPNNELLEKLKSNIEVR 538
Db 481 VALEGALKKEISYTHAEAYAGELKHGPLALVDSMPVTVVAPNNELVEKLKSNLQEV 540

Qy 539 ARGQLYVFADQDAGFVSSDNMHIEMPHVEEVIAPITVPLQLLAYHVALIKGTVDQ 598
Db 541 ARGQLYVFADQDAGFVSSDNMHIEMPHVEEVIAPITVPLQLLAYHVALIKGTVDQ 600

Qy 599 RNLAKSVTVE 609
Db 601 RNLAKSVTVE 611

RESULT 9
A84933
Glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) [imported] - Buc
N;Alternate names: D-fructose-6-phosphate amidotransferase
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 28-Jul-2003
C;Accession: A84933
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A;Reference number: A84930; MUID:20445173; PMID:10993077
A;Accession: A84933
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-621 <STO>
A;Cross-references: UNIPARC:UPI000005E424; GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: glmS; BU026
C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C;Keywords: aminotransferase; isomerase
Query Match 60.5%; Score 1868; DB 2; Length 621;

Best Local Similarity 59.1%; Pred. No. 8.8e-113;
Matches 361; Conservative 116; Mismatches 130; Indels 4; Gaps 3;
QY 1 MCGIVGATAQDVABILLGRLRLEVRGYDSAGLAVDAEGHMTLRLRLGKVMQLAQAAE 60
DB 13 MCGIVAAVTOBNIAFLIDGKLEVRGYDSGLAVIDNKNIVIRICVGNELIKTN 72
QY 61 EHLPGGTGIAHTRWATHGEPSEVNAHPHSEHIVVHNGIENHEPRLKARGYTFV 120
DB 73 KKKILSGVAVHTRWATHGKSKENTPHISSNIIIVHNGIENNSTLRLGFLKKQGYFS 132
QY 121 SETDTEVIAHLVNMEL-KQGTTLREAVLRAIPQLRGAYGTVIMDSRHPDITLLAARGSP 179
DB 133 SDTDEVIHLHWEQNKXDSLKIVQNSIKKLDGNSVMVIDQNNPSKLIARAAGSP 192
QY 180 VIGLGMENFIASQALALLPVRFFILEGDIABETTRSVNTPDKTGAEBKQDIESNL 239
DB 193 IIGLGTENFIASQIALHVTKRFIYLEGDIAIVARKEINIFNKNNSIIQREEVVNSI 252
QY 240 QYDAGDKGIVRYHMOKEIYEQPNAIKNTLTGRISH-CQVDLSELGPNADLLEKSKVEHIOI 298
DB 253 EYKSAKKGKRYNKEIHPQKSIKNTLNKRLNSKNVHFSSELGKKNFIYNTHEIOI 312
QY 299 LACTSYNSGMVSRWYFESLAGIPCDVEIASFPRYKSAVRRNSLMTITLSQSGETADTLA 358
DB 313 VACGTSYNAAMVSRWYFEEALANIPCDVEIASFSSRLKLVYRKSLITLSQSGETADTILS 372
QY 359 GLRLSKELGYLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTQLTVLLMLVA 418
DB 373 ALRYSKKLGYLGNLTICNMKSSSLVRESDFYITKAGLEIGVASTKFTTQLTVLLMLVA 432
QY 419 KLSRLKGLDASIEHDIYHGLQALPSRIEQMLSDQKRIEALAEFSDKHALLFLGRGDQY 478
DB 433 KIINSKKNNTSKRIIVQTLISILPVRLEELKXQILQDMANTLANKNMLFLGRNQRP 492
QY 479 IALEGALKKEISYIHAEEAAGELKHGPLALIDADMPVIVVAPNELLKLSNIEEVR 538
DB 493 IAMEGALKKEISYIHAEEAPSGELKHGPLALIDKNIPVIMTAPENSLEKKNKNIKEIC 552
QY 539 ARGQQLVFPADQAGFVSSDNMHIEMPHVEEVIPIFTVPLQLLAYHVALIKGTDVDO 598
DB 553 SRGIVTVFSNQ8--FDYEENINTIKLPYVEELIPIFTIPLQLPAYYVALKGRDIDQ 610
QY 599 PRNLAKSVTVE 609
DB 611 PRHLAKSVTVE 621

RESULT 10

E71272
Glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) glms - syphilis
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: E71272
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; UID:98332770; PMID:9665876
A:Accession: E71272
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-635 <COL>
A:Cross-references: UNIPROT:083833; UNIPARC:UPI0000164AEC; GB:AE001256; GB:AE000520; NID
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0861
C:Superfamily: Glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C:Keywords: aminotransferase; isomerase
F:2-635/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predi
F:2/Active site: Cys #status predicted

Query Match 55.2%; Score 1702; DB 2; Length 635;
Best Local Similarity 54.0%; Pred. No. 4.7e-102;
Matches 343; Conservative 98; Mismatches 168; Indels 26; Gaps 5;
QY 1 MCGIVGATAQDVABILLGRLRLEVRGYDSAGLAVDAEGHMTLRLRLGKVMQLAQAAE 60
DB 1 MCGIVGMVAGRVDSGLLEGRRLRLEVRGYDSAGIAGVDCALRLLRCEGRVQSLCALIG 60
QY 61 EHLPGGTGIAHTRWATHGEPSEVNAHPHSEHIVVHNGIENHEPRLKARGYTFV 120
DB 61 QSPLCGTGIAHTRWATHGKPCAAAHPCSESVAIVHNGIVENHRSIREMLVTGYPFH 120
QY 121 SETDTEVIAHLVNMELKOGGTLREAVLRAIPQLRGAYGTVIMDSRHPDITLLAARGSP 180
DB 121 SQTDEVLHLHWEIYTHALLAVKVLTVQVRGTGYLLCWDAAASPGRLIAAARGSP 180
QY 181 IGLGMENFIASQALALLPVRFFILEGDIABETTRSVNIPDKTGAEBKQDIESNLQ 240
DB 181 VGLGCGENFVSDPLALAHVTRQFYLEGDIADVHRDVCVHDAQGNVAVPVVYQMQ 240
QY 241 YDAGDKGIVRYHMOKEIYEQPNAIKNTLTGRISHGQVDLSEL-----GPN-----D 287
DB 241 LCTQDKGTHRHMHQEIWQPHAIRHTLNAVMSFSSSSRAQVRTFGEDVLDGTSCKTFE 300
QY 288 ELLSKVEHIQILACGTSYNSGMVSRWYFESLAGIPCDVEIASFPRYKSAVRRNSLMTIL 347
DB 301 RLFRITRVRIRIACGTSYHAGLVARYWFEAFAGVCGQVEIASEYRYRTSVVHAREIVLTI 360
QY 348 SQSGETADTLAAGRLSKELGYLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAF 407
DB 361 SQSGETADTLAALRLAKTQGVLCALICNGARSLTVRESDAVLTHAGSELGVASTKFT 420
QY 408 TQLTVLLMLVAKLSRLKG-LDASIEHDIYHGLQALPSRIEQMLSDQKRIEALAEFSDKH 466
DB 421 TQLVCLLVLTMIQAQAKKILTQEPEDALSAAQLRQPDQVEHVLCEADVARCARHFVHAQ 480
QY 467 HALFLGRGDQVPALLEGALKKEISYIHAEEAAGELKHGPLALIDADMPVIVVAPNNE- 525
DB 481 HALFLGRGELYPIAIESALKKEISYIHAEEAAGELKHGPLADVDQMPVVAITAPASPG 540
QY 526 -LLEKLKSNIEEVRARGQQLYVFPAD-----QDAGFVSSDNMHIEMPHVEEVIAP 574
DB 541 VLFEKMASNIEEVRARGGMLYIFTDVPERFGPCTPEADAPGACSQIVTVPSVSLTAP 600
QY 575 IFYTVPLQLLAYHVALIKGTDVQDQPRNLAKSVTVE 609
DB 601 IFYAVPLQLLAYHVALIKGTDIDQPRNLAKSVTVE 635

RESULT 11

A82844
Glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) [similarity] - X)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: A82844
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequenc
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; UID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: A82844
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-609 <SIM>
A:Cross-references: UNIPROT:Q9PH05; UNIPARC:UPI0000165AA; GB:AE003867; GB:AE003849; NID:
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; AJ
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Prohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XP0141
C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C;Keywords: aminotransferase; isomerase
F;2-609/Product: Glutamine-fructose-6-phosphate transaminase (isomerizing) #status predi
F;2/Active site: Cys #status predicted

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Query Match          54.9%; Score 1695; DB 2; Length 609;
Best Local Similarity 54.9%; Pred. No. 1.3e-101;
Matches 335; Conservative 103; Mismatches 170; Indels 2; Gaps 2;

Qy 1 MCGIVGAIARDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRRLGKVMQAQAAE 60
Db 1 MCGIVGAIARDVVPVLEGLKRLLEYRGYDSAGLAVLES-GSIRRVRTGRVAEMAAT 59

Qy 61 EPHLHGCTGTAHTRWATHGEPSEVNAHPHYS-EHIVVHNGIIEHHEPLREELKARGYTF 120
Db 60 QEGFTASLGIGHTRWATHGGVTEANHPHYSVSHGVLVHNGIIEHHEVQERLSALGVFQ 119

Qy 121 SETDTEVIAHLVNNELKQGGTLREAVLRATPOLRGAYGTVMDSRHPDTLAARSGSPLV 180
Db 120 SQDTEVIAHLIHYHMQGDDLLGALQCAVKALTGIYALAVMSAEFPCARMGCPLL 179

Qy 181 IGLGMGNFIASDQALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRODIESNLQ 240
Db 180 IGIQGEHLVASDISAVIQATQVIFLEDGDTAEIRRDGISIFNAEQCPVERPLHLSNVS 239

Qy 241 YDAGDKGIYRHYMOKETIEYQPNATKNTLTGRISHGQVDLSSELGNADLLSKVHEHIOILA 300
Db 240 LSSLELGEPRHFMQKETHQPRVLADTMEAAIDAAGFPFMLFGAQAESVFRGITGIQILA 299

Qy 301 CGTSYNGSMVSRVWFESLAGIPCDVEIASFPRYKRSVRRNSLMTLTSQGETADTLAGL 360
Db 300 CGTSYYAGLTARYWIEAIGLPCHVEIASERYKRYKAVNQHLVVTISQGETLDTLEAL 359

Qy 361 RLSKELGYLSLAI CNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQTLVLLMLVAKL 420
Db 360 KYAKALGHRHTLSICNAPDSAPRISELICVTRAGPEIGVASTKAFTTQLVWLFLQALVAL 419

Qy 421 SRLKG-LDASIEHDIVGLQALPSRIEOMLSQDKRIEALAEFSDKHALFLRGDQYPI 479
Db 420 GVLRGAVDAEHAAYLEQLRQLPCGVQOALNLEPQIAAWAECSFASRHHALFLGRGLHYPI 479

Qy 480 ALEGALKLKEISYIHAEAYAGELKHGKPLALIDAMPVIVVAPNNELLEKLKSNIEVRA 539
Db 480 ALEGALKLKEISYIHAEAYPAGELKHGKPLALVDMPPVVIAPNDSLEKVKSNMQSVRA 539

Qy 540 RGGOLYVFADQDAGFVSSDNMHIIEMPHVEVIAPIFYTVPLQLLAYHVALIKGTVDQOP 599
Db 540 RGGELFVFADQDSHFSSEGLHVIRTLRHTGVLSPLVHTIPVQLLAYHTALVRGTDVQKP 599

Qy 600 RNLAKSVTVE 609
Db 600 RNLAKSVTVE 609
```

RESULT 12

T45493
Glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) gims [similarity
N;Alternate names: glucosamine-6-phosphate synthase
C;Species: Thiobacillus ferrooxidans
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45493
R;Oppon, J.C.; Sarnovsky, R.J.; Craig, N.L.; Rawlings, D.E.
J. Bacteriol. 180, 3007-3012, 1998
A;Title: A Tn7-like transposon is present in the gims region of the obligately chemoaut

A;Reference number: Z22992; MUID:98269023; PMID:9603897
A;Accession: T45493
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-611 <OPP>
A;Cross-references: UNIPROT.Q56275; UNIPARC:UIP000016E22C; EMBL:AF032884; NID:G2653994;
A;Experimental source: ATCC 33020
C;Genetics:
A;Gene: gImS
C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C;Keywords: aminotransferase; isomerase

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Query Match          51.7%; Score 1597; DB 2; Length 611;
Best Local Similarity 52.8%; Pred. No. 2.7e-95;
Matches 325; Conservative 101; Mismatches 179; Indels 10; Gaps 5;

Qy 1 MCGIVGAIARDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRRLGKVMQAQAAE 60
Db 1 MCGIVGVSKTDLVPMILEGLQRLLEYRGYDSAGLAILGADADLLRVRSVGRVAELTAAV 60

Qy 61 EPHLHGCTGTAHTRWATHGEPSEVNAHPHYS-EHIVVHNGIIEHHEPLREELKARGYTF 119
Db 61 ERGLQGVGIGHTRWATHGGVRECNAHPMISHQIAVHNGIIEHHEPLRAHLEAAGYTF 120

Qy 120 VSETDTEVIAHLVNNELKQGGTLREAVLRATPOLRGAYGTVMDSRHPDTLAARSGSPL 179
Db 121 TSETDTEVIAHLVHHVYKOTAPDLFAATRRRAVGLRGAYATAVISSGDPETVCVARMGCP 180

Qy 180 VIGLGMGNFIASDQALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRODIESNL 239
Db 181 LLGVADDGHYFASDVAALLPVTRRVLYLEDGDVAMLQRTLRITDQAGASRQREHWSQL 240

Qy 240 QYDAGDKGIYRHYMOKETIEYQPNATKNTLTGRISHGQVDLSSEL-GPNADELLSKVHEHIOI 298
Db 241 SAAAVDLGPRHFMQKEIHEQPRAVADTLEGAL-NSQLDLDLWDGCAAMFRDVRDLV 299

Qy 299 LACGTSYNGSMVSRVWFESLAGIPCDVEIASFPRYKRSVRRNSLMTLTSQGETADTLAGL 358
Db 300 LASGTSHYATLVGRQWVESIVGIPAQAEELGHEYRYRDSIPDPRLQVLVVTLSQGETLDTFE 359

Qy 359 GLRLSKELGYLSLAI CNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQTLVLLMLVA 418
Db 360 ALBRKADLGHTRTLAICNVAESAIPRASALRFLTRAGPEIGVASTKAFTTQLAALYLLAL 419

Qy 419 KLSRLKGLDASIEHDIIVHG---LQALPSRIEOMLSQDKRIEALAEFSDKHALFLRG 474
Db 420 SLAKAPG---ASERCAGGSGFRLRQLPGSVQHALLNLEPQLQGWAAEFASKDHALFLRG 476

Qy 475 DQYPIALEGALKLKEISYIHAEAYAGELKHGKPLALIDAMPVIVVAPNNELLEKLKSN 534
Db 477 LHYPIALEGALKLKEISYIHAEAYPAGELKHGKPLALVDRMPVVVIAPNDRLLLEKLAAN 536

Qy 535 EEVRRAGGOLYVFADQDAGFVSSDNMHIIEMPHVEVIAPIFYTVPLQLLAYHVALIKGT 594
Db 537 QEYHARGGELYVFADSDSHFNAGSVHVMRLPRHAGLLSPVHAIPVQLLAYHAALVKGT 596

Qy 595 DVDQPRNLAKSVTVE 609
Db 597 DVDPRNLAKSVTVE 611
```

RESULT 13

H82022
Glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) NMA0276 [similar
N;Alternate names: glucosamine fructose-6-phosphate aminotransferase [aminomer]
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: H82022
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgensen, K.; Leather, S.; Moutle, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.
A;Reference number: A81775; MUID:20222556; PMID:10761919

A:Accession: H82022

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-612 <PAR>

A:Cross-references: UNIPROT:Q9JWN9; UNIPARC:UPI0000165682; GB:AL162752; GB:AL157959; NID

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: glmS; NMA0276

C:Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)

C:Keywords: aminotransferase; isomerase

F:2-612/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predicted

F:2/Active site: Cys #status predicted

Query Match
Best Local Similarity 50.9%; Score 1570.5; DB 2; Length 612;
Matches 325; Conservative 104; Mismatches 177; Indels 9; Gaps 9;

QY 1 MCGIVGAI-AQRDVAEILLEGRLREYGYDSAGLVVDAEGHMTLRRLRGKVMQAQA 59

DB 1 MCGIVGAI-RAHHNVVDFLTDLKRLRYGYDSSGIA-VNTDGKIKRVRRVGRVQLMEDAA 59

QY 60 EEHPLHGCGTGAHTRWATHGEPSEVNAHPHVS-EHIVVHNGIIEHPEELKARGYT 118

DB 60 REKISGGIGTGAHTRWATHGVTPEPNAHPHISGGMIAVHNGIIEHPESEKRLGLELYR 119

QY 119 FVSETDTEVIAHLVNMELKQ-GGTLREAVLRAIPQLRGAYGTVMDSRHPDTLLAARSGS 177

DB 120 FESQTDTEVIAHSINHEVAQNGKLFQAVQAVKRFHGAIAIAVIAQDKPELVVARMGC 179

QY 178 PLVTGLGNGENFIASDQALLPVTRRFIFLEBGDIABITRRSV-NIFDKTGAEVKRDIE 236

DB 180 PLLVALGDDEFTIASDVSAVIAFTRRVAYLEDGDIALASDGIKRLTDKSLPAERKVKV 239

QY 237 SNLQYDAGDKGIYRHYMOKIYEOPNAIKNTLTGRISHGQVDLSLGNADLLSKVEHI 296

DB 240 SELSLASLELGPYSHFWQKEIHEQPRAIADTAEVFLDGGFIP-ENFGKNAKSVFESIRSV 298

QY 297 QILACGTSYNGMVSRYWYFESLAGIPCDVEIASFEYRKSAVRRNSIMITLSQSGTADT 356

DB 299 KILACGTSYVAALTAQYKWLSEIAKIPSDVEIASERYSVIADPDQVLVITISQSGETLD 358

QY 357 LAGRLSKELGYLGLSLAICNVPSSLVRESDLAMTNAGTEIGVASTKFTTQLTVLLML 416

DB 359 MEALKYAKSLGHRHSLISICNVMESALPRESLLVLYTRAGAEIGVASTKFTTQLVALFGL 418

QY 417 VAKLSRLKGL-DASIEHDIHVGLQALPSRIEQMLSDOKRIEALAEFSDKHHLFLGRGD 475

DB 419 AVTLAKVRLGLVSEDEARYTEELRQLPGSVQHALLNLEPQIAAWAQFAKTSALFLGRGI 478

QY 476 QYPALLEGALKLKEISYTHAEYAAGELKHGPIALIDAMPVIVVAPNNLEKLKSNIE 535

DB 479 HYPALLEGALKLKEITYTHAEYAPAGELKHGPIALVDENMPVVIAPNDSLLDKVKANMQ 538

QY 536 EVPARGOLYVFADQADAGFVSSDNMHIEMP-HVEVIAPIFYTVPLQLLAHVHVALIKGT 594

DB 539 EVGARGELVFADLDSNFNATEGVHVIAPRRHVG-LSFVVHTPIPVQLLSYHVALARGT 597

QY 595 DVDQPRNLAKSVTVVE 609

DB 598 DVDKPRNLAKSVTVVE 612

RESULT 14

B81246

glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) NMB0031 [similar

N;Alternate names: glucosamine fructose-6-phosphate aminotransferase [misonomer]

C:Species: *Neisseria meningitidis*

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: B81246

R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiugnani, V.; Pizza, M.

Science 287, 1809-1915, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755; PMID:10710307

A:Accession: B81246

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-612 <TET>

A:Cross-references: UNIPROT:Q9KIP9; UNIPARC:UPI000016563D; GB:AE002361; GB:AE002098; NID

A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0031

C:Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)

C:Keywords: aminotransferase; isomerase

F:2-612/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predicted

F:2/Active site: Cys #status predicted

Query Match
Best Local Similarity 50.8%; Score 1566.5; DB 2; Length 612;
Matches 321; Conservative 104; Mismatches 182; Indels 7; Gaps 7;

QY 1 MCGIVGAI-AQRDVAEILLEGRLREYGYDSAGLVVDAEGHMTLRRLRGKVMQAQA 59

DB 1 MCGIVGAI-RAHHNVVDFLTDLKRLRYGYDSSGIA-VNTDGKIKRVRRVGRVQLMEDAA 59

QY 60 EEHPLHGCGTGAHTRWATHGEPSEVNAHPHVS-EHIVVHNGIIEHPEELKARGYT 118

DB 60 REKISGGIGTGAHTRWATHGVTPEPNAHPHISGGMIAVHNGIIEHPESEKRLGLELYR 119

QY 119 FVSETDTEVIAHLVNMELKQ-GGTLREAVLRAIPQLRGAYGTVMDSRHPDTLLAARSGS 177

DB 120 FESQTDTEVIAHSINHEVAQNGKLFQAVQAVKRFHGAIAIAVIAQDKPELVVARMGC 179

QY 178 PLVTGLGNGENFIASDQALLPVTRRFIFLEBGDIABITRRSV-NIFDKTGAEVKRDIE 236

DB 180 PLLVALGDDEFTIASDVSAVIAFTRRVAYLEDGDIALASDGIKRLTDKNGLPAERKVKV 239

QY 237 SNLQYDAGDKGIYRHYMOKIYEOPNAIKNTLTGRISHGQVDLSLGNADLLSKVEHI 296

DB 240 SELSLASLELGPYSHFWQKEIHEQPRAIADTAEVFLDGGFIP-ENFGKNAKSVFESIRSV 298

QY 297 QILACGTSYNGMVSRYWYFESLAGIPCDVEIASFEYRKSAVRRNSIMITLSQSGTADT 356

DB 299 KILACGTSYVAALTAQYKWLSEIAKIPSDVEIASERYSVIADSDQLVITISQSGETLD 358

QY 357 LAGRLSKELGYLGLSLAICNVPSSLVRESDLAMTNAGTEIGVASTKFTTQLTVLLML 416

DB 359 MEALKYAKSLGHRHSLISICNVMESALPRESLLVLYTRAGAEIGVASTKFTTQLVALFGL 418

QY 417 VAKLSRLKGL-DASIEHDIHVGLQALPSRIEQMLSDOKRIEALAEFSDKHHLFLGRGD 475

DB 419 AVTLAKVRLGLVSEDEARYTEELRQLPGSVQHALLNLEPQIAAWAQFAKTSALFLGRGI 478

QY 476 QYPALLEGALKLKEISYTHAEYAAGELKHGPIALIDAMPVIVVAPNNLEKLKSNIE 535

DB 479 HYPALLEGALKLKEITYTHAEYAPAGELKHGPIALVDENMPVVIAPNDSLLDKVKANMQ 538

QY 536 EVPARGOLYVFADQADAGFVSSDNMHIEMP-HVEVIAPIFYTVPLQLLAHVHVALIKGT 595

DB 539 EVGARGELVFADLDSNFNATEGVHVIAPRRHVGKLSFVVHTPIPVQLLAHVHVALARGTD 598

QY 596 DVDQPRNLAKSVTVVE 609

DB 599 DVDKPRNLAKSVTVVE 612

RESULT 15

AD3595

glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) [imported] - Bru

C:Species: *Brucella melitensis*

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: AD3595

R;DeiVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, T

; Mazur, M.; Goitsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessc

Search completed: August 7, 2006, 09:25:39
Job time : 27 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: August 7, 2006, 09:21:51 ; Search time 153 Seconds
(without alignments)
3681.925 Million cell updates/sec

Title: US-10-612-779-2

Perfect score: 3086

Sequence: 1 MCGIVGAIAQRDAEILLEG.....LIRGTDVDPRLAKSVTVE 609

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3086	100.0	609	2	Q2M847 escherichia
2	3081	99.8	608	1	GLMS ECOLI
3	3081	99.8	609	2	Q329F8 shigella dy
4	3079	99.8	609	2	Q31UM9 SHIDS
5	3077	99.7	608	1	GLMS ECO57
6	3077	99.7	608	1	GLMS SHIFL
7	3073	99.6	609	2	Q3YVN3 SHISS
8	3067	99.4	608	1	GLMS ECOL6
9	3058	99.1	608	1	GLMS SALPA
10	3058	99.1	609	2	Q57HY2 SALCH
11	3055	99.0	608	1	GLMS SALT1
12	3048	98.8	608	1	GLMS SALT1
13	2681.5	86.9	609	1	GLMS ERWCT
14	2677	86.7	608	1	GLMS YERPE
15	2677	86.7	608	1	GLMS YERPS
16	2565	83.1	608	1	GLMS PHOLL
17	2546.5	82.5	610	2	Q2NQ83 SODGL
18	2274.5	73.7	610	2	Q4QNB6 HAEI8
19	2265.5	73.4	609	1	GLMS HABIN
20	2261.5	73.3	609	1	GLMS VIBF1
21	2259.5	73.2	609	1	GLMS VIBCH
22	2245.5	72.8	609	1	GLMS PHOPR
23	2232.5	72.3	609	1	GLMS VIBPA
24	2224.5	72.1	609	1	GLMS VIBVU
25	2222.5	72.0	609	1	GLMS VIBVY
26	2212.5	71.7	610	2	Q3EGX5 ACTSC
27	2197.5	71.2	609	1	GLMS PASMU
28	2180.5	70.7	610	2	Q47UE2 COLP3
29	2159	70.0	609	2	Q338I7 shewanella
30	2159	70.0	609	2	Q3P1V9 9GAMM
31	2156	69.9	609	2	Q3Q8I9 9GAMM

RESULT 1

ID	Q2M847_ECOLI	Q2M847_ECOLI	PRELIMINARY;	PRT;	609 AA.
AC	Q2M847;				
DT	21-FEB-2006,	integrated into UniProtKB/TrEMBL.			
DT	21-FEB-2006,	sequence version 1.			
DT	07-MAR-2006,	entry version 2.			
DE	L-glutamine:D-fructose-6-phosphate	aminotransferase.			
GN	Name=glms;				
OS	Escherichia coli W3110.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria;	Enterobacteriales;			
OC	Enterobacteriaceae; Escherichia.				
OX	NCBI_TaxID=316407;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=K-12;				
RX	MEDLINE=81053692; PubMed=6159575;				
RA	Smith D.R., Calvo J.M.;				
RT	"Nucleotide sequence of the E coli gene coding for dihydrofolate reductase."				
RL	Nucleic Acids Res. 8:2255-2274(1980).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=K-12;				
RA	Sekiguchi T., Ortega-Cesena J., Nosoh Y., Ohashi S., Tauda K., Kanaya S.;				
RT	"DNA and amino-acid sequences of 3-isopropylmalate dehydrogenase of Bacillus coagulans. Comparison with the enzymes of Saccharomyces cerevisiae and Thermus thermophilus."				
RL	Biochim. Biophys. Acta 867:36-44(1986).				
RN	[3]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=K-12;				
RA	Chen H., Sun Y., Stark T., Beattie W., Moses R.E.;				
RT	"Nucleotide sequence and deletion analysis of the polB gene of Escherichia coli."				
RL	DNA Cell Biol. 9:613-635(1990).				
RN	[4]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=K-12;				
RA	Smallshaw J.E., Kelln R.A.;				
RT	"Cloning, nucleotide sequence and expression of the Escherichia coli K-12 pyrh gene encoding UMP kinase."				
RL	Genetics (Life Sci. Adv.) 11:59-65(1992).				
RN	[5]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=K-12;				
RA	Havashi K., Morooka N., Yamamoto Y., Fujita K., Isono K., Choi S., Ohtsubo E., Baba T., Wanner B.L., Mori H., Horiuchi T.;				
RT	"Highly accurate genome sequences of Escherichia coli K-12 strains MG1655 and W3110."				
RL	Mol. Syst. Biol. 0:0-0(2006).				
RN	[6]				
RP	NUCLEOTIDE SEQUENCE.				

Q2xlg5 shewanella
Q2zql1 shewanella
Q366r1 9GAMM
Q2z4d9 shewanella
Q35v59 shewanella
Q7vkk4 h glucosami
Q8cx33 s glucosami
Q3ky7 shewanella
Q5qzhs i glucosami
Q3csc7 pseudoalter
Q3ik37 pseudoalter
Q2xhy7 pseudomonas
Q3k445 pseudomonas
Q88bx8 p glucosami

ALIGNMENTS

RC STRAIN=K-12;
RX PubMed=16397293; DOI=10.1093/nar/gkj150;
RA Riley M., Abe T., Arnaud M.B., Berlyn M.K., Blattner F.R.,
RA Chaudhuri R.R., Glaser J.D., Horiuchi T., Kessler I.M., Kosuge T.,
RA Mori H., Perna N.T., Plunkett G. III, Rudd K.E., Serres M.H.,
RA Thomas G.H., Thomson N.R., Wishart D., Wanner B.L.;
RT "Escherichia coli K-12: a cooperatively developed annotation snapshot-
RT -2005";
RL Nucleic Acids Res. 34:1-9(2006).
RN [7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=97349980; PubMed=9205837; DOI=10.1093/dnares/4.2.91;
RA Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT -K12 genome corresponding to 50.0-68.8 min on the linkage map and
RT analysis of its sequence features";
RL DNA Res. 4:91-113(1997).
RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=97251359; PubMed=9097040; DOI=10.1093/dnares/3.6.379;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
RA Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map";
RL DNA Res. 3:379-392(1996).
RN [9]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=97251357; PubMed=9097039; DOI=10.1093/dnares/3.6.363;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map";
RL DNA Res. 3:363-377(1996).
RN [10]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=97094878; PubMed=8940112; DOI=10.1074/jbc.271.49.31145;
RA Arn E.A., Abelson J.N.;
RT "The 2'-5' RNA ligase of Escherichia coli. Purification, cloning, and
RT genomic disruption";
RL J. Biol. Chem. 271:31145-31153(1996).
RN [11]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=97061202; PubMed=8905232; DOI=10.1093/dnares/3.3.137;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Mizobuchi K.,
RA Mori H., Moromura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map";
RL DNA Res. 3:137-155(1996).
RN [12]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=94261430; PubMed=8202364;
RA Fujita N., Mori H., Yura T., Ishihama A.;
RT "Systematic sequencing of the Escherichia coli genome: analysis of the
RT 2.4-4.1 min (110,917-193,643 bp) region";
RL Nucleic Acids Res. 22:1637-1639(1994).
RN [13]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=94240115; PubMed=8183897;
RA Janosi L., Shimizu I., Kaji A.;
RT "Ribosome recycling factor (ribosome releasing factor) is essential
RT for bacterial growth";
RL Proc. Natl. Acad. Sci. U.S.A. 91:4249-4253(1994).
RN [14]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=94124004; PubMed=7904973; DOI=10.1016/0378-1119(93)90470-N;
RA Allikmets R., Gerrard B.C., Court D., Dean M.C.;
RT "Cloning and organization of the abc and mdl genes of Escherichia
RT coli: relationship to eukaryotic multidrug resistance";
RL Gene 136:231-236(1993).
RN [15]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=94018640; PubMed=8412694;
RA van Heeswijk W.C., Rabenberg M., Westerhoff H.V., Kahn D.D.;
RT "The genes of the glutamine synthetase adenylation cascade are not
RT regulated by nitrogen in Escherichia coli";
RL Mol. Microbiol. 9:443-458(1993).
RN [16]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=93259920; PubMed=8387890;
RA Zhao S., Sandt C.H., Feulner G., Vlazny D.A., Gray J.A., Hill C.W.;
RT "Rhs elements of Escherichia coli K-12: complex composites of shared
RT and unique components that have different evolutionary histories";
RL J. Bacteriol. 175:2799-2808(1993).
RN [17]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=93123180; PubMed=8419307;
RA Yamada M., Aasaka S., Saier M.H. Jr., Yamada Y.;
RT "Characterization of the gcd gene from Escherichia coli K-12 W3110 and
RT regulation of its expression";
RL J. Bacteriol. 175:568-571(1993).
RN [18]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=93116053; PubMed=1474579;
RA Cormack R.S., Mackie G.A.;
RT "Structural requirements for the processing of Escherichia coli 5 S
RT ribosomal RNA by RNase E in vitro";
RL J. Mol. Biol. 228:1078-1090(1992).
RN [19]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=93094132; PubMed=1459951;
RA Gervais F.G., Drapeau G.R.;
RT "Identification, cloning, and characterization of rcsF, a new
RT regulator gene for exopolysaccharide synthesis that suppresses the
RT division mutation fts284 in Escherichia coli K-12";
RL J. Bacteriol. 174:8016-8022(1992).
RN [20]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=K-12;
RX MEDLINE=93077430; PubMed=1447125;
RA Yamanaka K., Ogura T., Niki H., Hiraga S.;
RT "Identification and characterization of the smbA gene, a suppressor of
RT the mukB null mutant of Escherichia coli";
RL J. Bacteriol. 174:7517-7526(1992).
RN [21]
RP NUCLEOTIDE SEQUENCE.
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RX MEDLINE=93011013; PubMed=1396599;
RA Condon C., Phillips J., Fu Z.Y., Squires C., Squires C.L.;

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ID GLMS_ECOLI
AC P17169; P76745;
DT 01-AUG-1990, integrated into UniProtKB/Swiss-Prot.
DT 15-DEC-1998, sequence version 3.
DT 07-MAR-2006, entry version 70.
DE Glucosamine--fructose-6-phosphate aminotransferase (isomerizing)
DE (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-
DE phosphate amidotransferase) (G6P) (L-glutamine-D-fructose-6-phosphate
DE amidotransferase) (Glucosamine-6-phosphate synthase).
GN Name:glms; OrderedLocusNames:b3729;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=85121806; PubMed=6395859;
RA Walker J.E., Gay N.J., Saraste M., Eberle A.N.;
RT "DNA sequence around the Escherichia coli unc operon. Completion of
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RT the sequence of a 17 kilobase segment containing asnA, oriC, unc, glms
RL and phos.";
RN Biochem. J. 224:799-815(1984).
[2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=K12 / MGI655;
RX MEDLINE=93315143; PubMed=7686882;
RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli
RT genome: organizational symmetry around the origin of replication.";
RL Genomics 16:551-561(1993).
[3]
RP PROTEIN SEQUENCE OF 48-51; 218-230; 488-492; 504-507 AND 600-608.
RX MEDLINE=92007872; PubMed=1915361;
RA Golinski-Pimpaneau B., Badet B.;
RT "Possible involvement of Lys603 from Escherichia coli glucosamine-6-
RT phosphate synthase in the binding of its substrate fructose 6-
RL phosphate.";
RN Eur. J. Biochem. 201:175-182(1991).
[4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 489-608.
RX MEDLINE=82220022; PubMed=6283361;
RA Lichtenstein C., Brenner S.;
RT "Unique insertion site of Tn7 in the E. coli chromosome.";
RL Nature 297:601-603(1982).
[5]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 606-608.
RX MEDLINE=86215091; PubMed=3010949;
RA Gay N.J., Tybulewicz V.L.-J., Walker J.E.;
RT "Insertion of transposon Tn7 into the Escherichia coli glms
RT transcriptional terminator.";
RL Biochem. J. 234:111-117(1986).
[6]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 596-608.
RX MEDLINE=88086894; PubMed=2826397;
RA McKown R.L., Orle K.A., Chen T., Craig N.L.;
RT "Sequence requirements of Escherichia coli attTn7, a specific site of
RT transposon Tn7 insertion.";
RL J. Bacteriol. 170:352-358(1988).
[7]
RP CHARACTERIZATION.
RX MEDLINE=88281539; PubMed=3134953; DOI=10.1016/0300-9084(88)90073-9;
RA Dutka-Malen S., Mazodier P., Badet B.;
RT "Molecular cloning and overexpression of the glucosamine synthetase
RT gene from Escherichia coli.";
RL Biochimie 70:287-290(1988).
[8]
RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 1-240.
RX MEDLINE=96434326; PubMed=8805567; DOI=10.1016/S0969-2126(96)00087-1;
RA Tsupov M.N., Obmolova G., Butterworth S., Badet-Denisot M.-A.,
RA Badet B., Polikarpov I., Littlechild J.A., Teplovskov A.;
RT "Substrate binding is required for assembly of the active conformation
RT of the catalytic site in Ntn amidotransferases: evidence from the 1.8-
RT A crystal structure of the glutaminase domain of glucosamine 6-
RT phosphate synthase.";
RL Structure 4:801-810(1996).
[9]
RP X-RAY CRYSTALLOGRAPHY (1.57 ANGSTROMS) OF 243-608.
RX MEDLINE=98416699; PubMed=9739095; DOI=10.1016/S0969-2126(98)00105-1;
RA Teplovskov A., Obmolova G., Badet-Denisot M.-A., Badet B.,
RA Polikarpov I.;
RT "Involvement of the C terminus in intramolecular nitrogen channeling
RT in glucosamine 6-phosphate synthase: evidence from a 1.6-A crystal
RT structure of the isomerase domain.";
RL Structure 6:1047-1055(1998).
[10]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 241-608.
RX MEDLINE=99190083; PubMed=10091662;
RA Teplovskov A., Obmolova G., Badet-Denisot M.A., Badet B.;
RT "The mechanism of sugar phosphate isomerization by glucosamine 6-
RT phosphate synthase.";
RL Protein Sci. 8:596-602(1999).
CC -!- FUNCTION: Catalyzes the first step in hexosamine metabolism,
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converting fructose-6P into glucosamine-6P using glutamine as a nitrogen source.
-I- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-glutamate + D-glucosamine 6-phosphate.
-I- SUBUNIT: Homodimer.
-I- INTERACTION: P00957:alaS; N5Exp=1; IntAct=EBI-551022, EBI-544061; P08622:dnaJ; N5Exp=1; IntAct=EBI-551022, EBI-545285; P76552:eutH; N5Exp=1; IntAct=EBI-551022, EBI-551031; P62615:apeE; N5Exp=1; IntAct=EBI-551022, EBI-562202; P61175:rpIV; N5Exp=1; IntAct=EBI-551022, EBI-542255; P21166:crkH; N5Exp=1; IntAct=EBI-551022, EBI-550268; P76093:yndB; N5Exp=1; IntAct=EBI-551022, EBI-551038; P33366:yohD; N5Exp=1; IntAct=EBI-551022, EBI-551046; -I- SUBCELLULAR LOCATION: Cytoplasm.
-I- SIMILARITY: In the C-terminal section; belongs to the SIS family. GPAT subfamily.

-I- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.

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EMBL; X01631; CAA25785.1; -; Genomic DNA.
EMBL; L10328; AAA62080.1; -; Genomic DNA.
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EMBL; M18980; AAA23836.1; -; Genomic DNA.
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DR InterPro; IPR000583; GATase_2.
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DR Pfam; PF00310; GATase_2; 1.
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KW Direct protein sequencing; Glutamine amidotransferase; Transferase.
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Matches 508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 06-DEC-2005, sequence version 1.
DE L-glutamine:D-fructose-6-phosphate aminotransferase.
GN Name=glms; OrderedLocusNames=SDY_4019;
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OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=300267;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16275786; DOI=10.1093/nar/gki954;
RA Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
RT agents of bacillary dysentery."
RL Nucleic Acids Res. 33:6445-6458(2005).
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CC -----
CC EMBL: CP000034; AB63937.1; -; Genomic_DNA.
DR GO: GO:0005377; C:cytoplasm; IEA.
DR GO: GO:0004360; F:glutamine-fructose-6-phosphate transaminase. . ; IEA.
DR GO: GO:0005529; F:sugar binding; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0016051; P:carbohydrate biosynthesis; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
KW Aminotransferase; Complete proteome; Transferase.
SQ SEQUENCE 609 AA; 66904 MW; 6373301513227484 CRC64;

Query Match 99.8%; Score 3081; DB 2; Length 609;
Best Local Similarity 99.8%; Pred. No. 5.8e-186;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIAORDVAEILLEGRLRLEYRGYDSAGLAVVDAGHMTLRRLRGKVMQAAAE 60
Db 1 MCGIVGAIAORDVAEILLEGRLRLEYRGYDSAGLAVVDAGHMTLRRLRGKVMQAAAE 60

Qy 61 EHPLHGCTGTAHTRWATHGSPSEVNAHPHVSEHIVVHNGIIEHNEHPLRELKARGYTFV 120
Db 61 EHPLHGCTGTAHTRWATHGSPSEVNAHPHVSEHIVVHNGIIEHNEHPLRELKARGYTFV 120

Qy 121 SETDTEVIAHVNWELKOGGTLREAVLRATPOLRGAYGTVMDSRHPDTHLAARSGSPV 180
Db 121 SETDTEVIAHVNWELKOGGTLREAVLRATPOLRGAYGTVMDSRHPDTHLAARSGSPV 180

Qy 181 IGLGMGNFTASDQALLPTVRRIFLEEGDIAETRRSVNIFDKTGAEVKRODIESNLQ 240
Db 181 IGLGMGNFTASDQALLPTVRRIFLEEGDIAETRRSVNIFDKTGAEVKRODIESNLQ 240

Qy 241 YDAGDKGIYRHYMQKIYEQPNAIKNTLTGRISHGQVDLSLGNPADELLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKIYEQPNAIKNTLTGRISHGQVDLSLGNPADELLSKVEHIQILA 300
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Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASEFRYKRSVARRNSLMTLSQSGETADTLAGL 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASEFRYKRSVARRNSLMTLSQSGETADTLAGL 360
Qy 361 RLSKEILGYLGSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTOLTVLMLVAKL 420
Db 361 RLSKEILGYLGSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTOLTVLMLVAKL 420
Qy 421 SRLKGLDASTIEHDI VHGLQALPSRIEOMLSQDKRIEALAEDFSCKHALFLRGDQYPIA 480
Db 421 SRLKGLDASTIEHDI VHGLQALPSRIEOMLSQDKRIEALAEDFSCKHALFLRGDQYPIA 480
Qy 481 LEGALKLKEISYTHAEYAAAGELKHGPLALIDADMPVIVVAPNNLEKLNIEEVRAR 540
Db 481 LEGALKLKEISYTHAEYAAAGELKHGPLALIDADMPVIVVAPNNLEKLNIEEVRAR 540
Qy 541 GGQLYVPADQDAGFVSSDNMHIEMPHVEEVIAPFYTVPLQLLAYHVALIKGTDVDDOPR 600
Db 541 GGQLYVPADQDAGFVSSDNMHIEMPHVEEVIAPFYTVPLQLLAYHVALIKGTDVDDOPR 600
Qy 601 NLAKSVTVTE 609
Db 601 NLAKSVTVTE 608

RESULT 4
Q31UM9_SHIDS
ID Q31UM9_SHIDS PRELIMINARY; PRT; 609 AA.
AC Q31UM9;
DT 06-DEC-2005, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 1.
DE L-glutamine:D-fructose-6-phosphate aminotransferase.
GN Name=glms; OrderedLocusNames=SBO_3758;
OS Shigella boydii serotype 4 (strain Sb227).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=300268;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16275786; DOI=10.1093/nar/gki954;
RA Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
RT agents of bacillary dysentery."
RL Nucleic Acids Res. 33:6445-6458(2005).
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CC -----
CC EMBL: CP000036; AB68229.1; -; Genomic_DNA.
DR GO: GO:0005377; C:cytoplasm; IEA.
DR GO: GO:0004360; F:glutamine-fructose-6-phosphate transaminase. . ; IEA.
DR GO: GO:0005529; F:sugar binding; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
DR GO: GO:0016051; P:carbohydrate biosynthesis; IEA.
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
KW Aminotransferase; Complete proteome; Transferase.
SQ SEQUENCE 609 AA; 66898 MW; 989B94DC79C348D4 CRC64;

Query Match 99.8%; Score 3079; DB 2; Length 609;
Best Local Similarity 99.7%; Pred. No. 7.7e-186;
Matches 607; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIAORDVAEILLEGRLRLEYRGYDSAGLAVVDAGHMTLRRLRGKVMQAAAE 60
Db 1 MCGIVGAIAORDVAEILLEGRLRLEYRGYDSAGLAVVDAGHMTLRRLRGKVMQAAAE 60

Qy 61 EHPLHGCTGTAHTRWATHGSPSEVNAHPHVSEHIVVHNGIIEHNEHPLRELKARGYTFV 120
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Qy 302 GTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKRSVARRNSLMTLSQSGETADTLAGLR 361
Db 301 GTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKRSVARRNSLMTLSQSGETADTLAGLR 360
Qy 362 LSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFITLTQLTVLLMLVAKLS 421
Db 361 LSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFITLTQLTVLLMLVAKLS 420
Qy 422 RLKGLDASIEHDIHVHGLQALPSRIEOMLSQDKRIEALAEAFSDKHAFILGRGDQYPIAL 481
Db 421 RLKGLDASIEHDIHVHGLQALPSRIEOMLSQDKRIEALAEAFSDKHAFILGRGDQYPIAL 480
Qy 482 EGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEEVRARG 541
Db 481 EGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEEVRARG 540
Qy 542 GOLYVFADQAGFVSSDNMHIEMPHVEEVIAPFYTPVPLQLLAYHVALLKGTDDVQPRN 601
Db 541 GOLYVFADQAGFVSSDNMHIEMPHVEEVIAPFYTPVPLQLLAYHVALLKGTDDVQPRN 600
Qy 602 LAKSVTVE 609
Db 601 LAKSVTVE 608

RESULT 6
GLMS_SHIFL STANDARD; PRT; 608 AA.
AC Q831Y4; Q7B299;
DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
DT 30-AUG-2005, sequence version 2.
DT 07-MAR-2006, entry version 22.
DE Glucosamine-6-phosphate aminotransferase (isomerizing)
DE (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-
DE phosphate amidotransferase) (GPAT) (L-glutamine-D-fructose-6-phosphate
DE amidotransferase) (Glucosamine-6-phosphate synthase).
GN Name=glms; OrderedLocusNames=SF3809, S3959;
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=623;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12394590; DOI=10.1093/nar/gkf566;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Yu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157."
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T."
RL Infect. Immun. 71:2775-2786(2003).
CC -1- FUNCTION: Catalyzes the first step in hexosamine metabolism,
CC converting fructose-6P into glucosamine-6P using glutamine as a
CC nitrogen source (By similarity).
CC -1- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-
CC glutamate + D-glucosamine 6-phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC -1- SIMILARITY: In the C-terminal section; belongs to the SIS family.
CC GPAT subfamily.

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CC -1- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AE005674; AA045249.1; -; Genomic DNA.
DR EMBL; AE016991; AAP18948.1; -; Genomic DNA.
DR HSSP; P17169; 1JXA.
DR SMR; Q831Y4; 1-239, 243-608.
DR GenomeReviews; AE014073 GR; S3959.
DR GenomeReviews; AE005674 GR; SF3809.
DR BioCyc; SFLE198214:AA045249.1-MONOMER; -.
DR HAMAP; MF 00164; -; 1.
DR InterPro; IPR000583; GATase_2.
DR InterPro; IPR005855; Glms_trans.
DR InterPro; IPR001347; SIS_trans.
DR Pfam; PF00310; GATase_2; 1.
DR Pfam; PF01380; SIS; 2.
DR TIGRFAMs; TIGR01135; glms; 1.
DR PROSITE; PS00443; GATASE_TYPE_II; 1.
DR AminoTransferase; Complete proteome; Glutamine amidotransferase;
KW Transferase.
FT INIT_MET 0 0 By similarity.
FT CHAIN 1 608 Glucosamine--fructose-6-phosphate
FT aminotransferase [isomerizing].
FT /FTid=PRO_0000135377.
FT REGION 1 240 Glutamine amidotransferase.
FT ACT_SITE 1 1 GATase (By similarity).
FT ACT_SITE 603 603 Isomerization Fru-6P (By similarity).
SQ SEQUENCE 608 AA; 66735 MW; B0CEDA38B6F00F7D CRC64;

Query Match 99.7%; Score 3077; DB 1; Length 608;
Best Local Similarity 99.8%; Pred. No. 1e-185;
Matches 607; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CGIVGAIAQRDVAEILLEGRLLERYGYDSAGLAVVDAEGHMTLRRLRGKVMQAQAAEE 61
Db 1 CGIVGAIAQRDVAEILLEGRLLERYGYDSAGLAVVDAEGHMTLRRLRGKVMQAQAAEE 60
Qy 62 HPLHGGTGIAHTRWATHGEPSEVNAHPHVSEHVVVHNGIIENHEPRLBELKARGYTFVS 121
Db 61 HPLHGGTGIAHTRWATHGEPSEANAPHVSEHVVVHNGIIENHEPRLBELKARGYTFVS 120
Qy 122 ETDEVIHLVNLWELKGGTLREAVLRRAIPOLRGAGVTIVMDSRHPTDTLAARSGSLVI 181
Db 121 ETDEVIHLVNLWELKGGTLREAVLRRAIPOLRGAGVTIVMDSRHPTDTLAARSGSLVI 180
Qy 182 GLGMGFNTASDQALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRDIESNLQY 241
Db 181 GLGMGFNTASDQALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRDIESNLQY 240
Qy 242 DAGDKGIYRHYMQEYEQPNALKNLTGRI SHGQVDLSLGPNADELLSKVEHIQILAC 301
Db 241 DAGDKGIYRHYMQEYEQPNALKNLTGRI SHGQVDLSLGPNADELLSKVEHIQILAC 300
Qy 302 GTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKRSVARRNSLMTLSQSGETADTLAGLR 361
Db 301 GTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKRSVARRNSLMTLSQSGETADTLAGLR 360
Qy 362 LSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFITLTQLTVLLMLVAKLS 421
Db 361 LSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFITLTQLTVLLMLVAKLS 420
Qy 422 RLKGLDASIEHDIHVHGLQALPSRIEOMLSQDKRIEALAEAFSDKHAFILGRGDQYPIAL 481
Db 421 RLKGLDASIEHDIHVHGLQALPSRIEOMLSQDKRIEALAEAFSDKHAFILGRGDQYPIAL 480
Qy 482 EGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEEVRARG 541
Db 481 EGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEEVRARG 540
Qy 542 GOLYVFADQAGFVSSDNMHIEMPHVEEVIAPFYTPVPLQLLAYHVALLKGTDDVQPRN 601

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Db 541 GQLYVFADQDAGFVSSDNMHIEPHVEEVIAPFYTVPLQLLAYHVALIKGTDVDQPRN 600
QY 602 LAKSVTVE 609
Db 601 LAKSVTVE 608

RESULT 7
Q3YVN3_SHISS PRELIMINARY; PRT; 609 AA.
ID Q3YVN3;
AC Q3YVN3;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE L-glutamine-D-fructose-6-phosphate aminotransferase.
GN Name=glms; OrderedLocNames=SSO_3890; ORFNames=SSO_3890;
OS Shigella sonnei (strain S046).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Shigella.
OX NCBI_TaxID=300269;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=16275786; DOI=10.1093/nar/gki954;
RA Yang J., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
RA Wang F., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,
RA Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
RA Qiang B., Hou Y., Yu J., Jin Q.;
RT "Genome dynamics and diversity of Shigella species, the etiologic
RT agents of bacillary dysentery.";
RL Nucleic Acids Res. 33:6445-6458 (2005).
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CC -----
EMBL: CP000038; AA290429.1; -; Genomic_DNA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0004360; F:glutamine-fructose-6-phosphate transaminase. .; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016051; P:carbohydrate biosynthesis; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000583; GATase_2.
DR InterPro; IPR005855; Glms_trans.
DR InterPro; IPR001347; SIS.
DR Pfam; PF00310; GATase_2; 1.
DR Pfam; PF01380; SIS; 2.
DR TIGRFAMs; TIGR01135; glms; 1.
DR PROSITE; PS00443; GAVASE_TYPE_II; UNKNOWN 1.
KW Aminotransferase; Complete proteome; Transferase.
SQ SEQUENCE 609 AA; 66844 MW; 9BE75125C4D348D4 CRC64;

Query Match 99.6%; Score 3073; DB 2; Length 609;
Best Local Similarity 99.7%; Pred. No. 1.9e-185;
Matches 607; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCGIVCAIQRDVAETLLRGLRLRYGYDSAGLAVDVAEGHMTLRRLGKVMQLQAAR 60
Db 1 MCGIVCAIQRDVAETLLRGLRLRYGYDSAGLAVDVAEGHMTLRRLGKVMQLQAAR 60
QY 61 EHPHLCGTGTATRWATHGEPSEVNAPHVSEHVVVHNGIIEHPLEELKARGYTFV 120
Db 61 EHPHLCGTGTATRWATHGEPSEVNAPHVSEHVVVHNGIIEHPLEELKARGYTFV 120
QY 121 SETDTEVIAHLNVNELKQGGTLREAVLRAIPOLRGAYGTVMDSRHPDPTLLAARSGSLV 180
Db 121 SETDTEVIAHLNVNELKQGGTLREAVLRAIPOLRGAYGTVMDSRHPDPTLLAARSGSLV 180
QY 181 IGLGNGENFIADQLALLPVRFRFLEEGDIAETTRRSVNFDKTGAEVKQDIESNLQ 240
Db 181 IGLGNGENFIADQLALLPVRFRFLEEGDIAETTRRSVNFDKTGAEVKQDIESNLQ 240
QY 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSLGNADLLSKVEHIQILA 300
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Db 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSLGNADLLSKVEHIQILA 300
QY 301 CGTSYNSGWSRYWFESLAGIPCDVEIASERFYRKSAVRNSLMITLSQSGTADTLAGL 360
Db 301 CGTSYNSGWSRYWFESLAGIPCDVEIASERFYRKSAVRNSLMITLSQSGTADTLAGL 360
QY 361 RLSKELGYLGLAICNVPGSSILVRESDLALMTNAGTEIGVASTKATPTQLTVLLMLVAKL 420
Db 361 RLSKELGYLGLAICNVPGSSILVRESDLALMTNAGTEIGVASTKATPTQLTVLLMLVAKL 420
QY 421 SRLKGLDASIEHDI VHGLQALPSRIEQLMSQDKRIEALAEFSDXKHALFLGRGQDYPIA 480
Db 421 SRLKGLDASIEHDI VHGLQALPSRIEQLMSQDKRIEALAEFSDXKHALFLGRGQDYPIA 480
QY 481 LEGALKLKEISYIHAEAYAGELKHGCPALADADMPVIVVAPNNELLEKLKSNIEVRAR 540
Db 481 LEGALKLKEISYIHAEAYAGELKHGCPALADADMPVIVVAPNNELLEKLKSNIEVRAR 540
QY 541 GGQLYVFADQDAGFVSSDNMHIEPHVEEVIAPFYTVPLQLLAYHVALIKGTDVDQPR 600
Db 541 GGQLYVFADQDAGFVSSDNMHIEPHVEEVIAPFYTVPLQLLAYHVALIKGTDVDQPR 600
QY 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 8
GLMS_ECOL6
ID GLMS_ECOL6 STANDARD; PRT; 608 AA.
AC Q8PBT4;
DT 06-JUN-2003, integrated into UniProtKB/Swiss-Prot.
DT 06-JUN-2003, sequence version 2.
DT 07-MAR-2006, entry version 17.
DE Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
DE (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-
DE phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate
DE amidotransferase) (Glucosamine-6-phosphate synthase).
GN Name=glms; OrderedLocNames=c4654;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Raeko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
CC -!- FUNCTION: Catalyzes the first step in hexosamine metabolism,
CC converting fructose-6P into glucosamine-6P using glutamine as a
CC nitrogen source (By similarity).
CC -!- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-
CC glutamate + D-glucosamine 6-phosphate.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC -!- SIMILARITY: In the C-terminal section; belongs to the SIS family.
CC GFAT subfamily.
CC -!- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
EMBL: AE016769; AA03086.1; -; Genomic_DNA.
DR HSSP; P17169; IMOS.
DR SMR; Q8PBT4; 1-239, 243-608.
DR GenomeReviews; AB014075_GR; c4654.
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DR BioCyc; EC01199310:C4654-MONOMER; -.
DR HAMAP; MF 00164; -.
DR InterPro; IPR000583; GATase.2.
DR InterPro; IPR005855; GlnS_trans.
DR InterPro; IPR001347; SIS.
DR Pfam; PF00310; GATase_2; 1.
DR Pfam; PF01380; SIS; 2.
DR TIGRFAMs; TIGR01135; glns; 1.
DR PROSITE; PS00443; GATASE_TYPE_II; 1.
KW Amino transferase; Complete proteome; Glutamine amidotransferase;
KW Transferase.
FT INIT_MET 0 0 By similarity.
FT CHAIN 1 608 Glutamine--fructose-6-phosphate
FT aminotransferase [isomerizing].
FT FTID=PRO 0000135329.
FT REGION 1 240 Glutamine amidotransferase.
FT ACT_SITE 1 1 GATase (By similarity).
FT ACT_SITE 603 Isomerization Fru-6P (By similarity).
SQ SEQUENCE 608 AA; 66647 MW; 44DADB5D072C65D7 CRC64;

Query Match 99.4%; Score 3067; DB 1; Length 608;
Best Local Similarity 99.5%; Pred. No. 4.4e-185;
Matches 605; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGIVGAIAQRDVAAEILLEGRLRLRYGYDSAGLAVVDAEGHMTLRRLKGVQMLAQAAEE 61
DB 1 CGIVGAIAQRDVAAEILLEGRLRLRYGYDSAGLAVVDAEGHMTLRRLKGVQMLAQAAEE 60
QY 62 HPLHGCGTGAHTRWATHGEPSEVNAHPVSEHIVVHNGIENHPELREELKARGYTFVS 121
DB 61 HPLHGCGTGAHTRWATHGEPSEVNAHPVSEHIVVHNGIENHPELREELKARGYTFVS 120
QY 122 ETDTEVIAHLVNWELKOGGTLREAVLRATPOLRGAYGTWIMDSRHPDTLLAARSGSPLYI 181
DB 121 ETDTEVIAHLVNWELKOGGTLREAVLRATPOLRGAYGTWIMDSRHPDTLLAARSGSPLYI 180
QY 182 GLGWMGFNFIASDQALLPVTRRIFLEEGDIAETIRRSVNI FDKTGAEVKRGQDIENLQY 241
DB 181 GLGWMGFNFIASDQALLPVTRRIFLEEGDIAETIRRSVNI FDKTGAEVKRGQDIENLQY 240
QY 242 DAGDKGIYRHYMQEYIYEQPNAIKNTLTGRISHGQVDLSLGNADDELLSKVEHIQILAC 301
DB 241 DAGDKGIYRHYMQEYIYEQPNAIKNTLTGRISHGQVDLSLGNADDELLSKVEHIQILAC 300
QY 302 GTSYNSGMVSRVYFESLAGIPCDVEIASEFRYKSAVRNLSMITLSQSGETADTLAQLR 361
DB 301 GTSYNSGMVSRVYFESLAGIPCDVEIASEFRYKSAVRNLSMITLSQSGETADTLAQLR 360
QY 362 LSKELGYLGSALACNVPGSSLVRESDLALMTNAGTEIGVASTKAFITQTLTLLMLVAKLS 421
DB 361 LSKELGYLGSALACNVPGSSLVRESDLALMTNAGTEIGVASTKAFITQTLTLLMLVAKLS 420
QY 422 RLKGLDASIEHDIVHGLQALPSRIEQMLSQDKRIEALAEEDFSKHHALFLGRGDQYPIAL 481
DB 421 RLKGLDASIEHDIVHGLQALPSRIEQMLSQDKRIEALAEEDFSKHHALFLGRGDQYPIAL 480
QY 482 EGALKLKEISYTHAEYAYAGELKHGFLALIDAMPVIVVAPNNELLEKLKSNIEEVRAG 541
DB 481 EGALKLKEISYTHAEYAYAGELKHGFLALIDAMPVIVVAPNNELLEKLKSNIEEVRAG 540
QY 542 GOLYVFADODDAGFVSDNNMHI IEMPHVEEVIAPFVYTPVLPQLLAYHVALIKGTDVDPQRN 601
DB 541 GOLYVFADODDAGFVSDNNMHI IEMPHVEEVIAPFVYTPVLPQLLAYHVALIKGTDVDPQRN 600
QY 602 LAKSVTVE 609
DB 601 LAKSVTVE 608

RESULT 9
GLMS_SALPA STANDARD; PRT; 608 AA.
ID_GLMS_SALPA AC Q5PKV9;

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DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
DT 30-AUG-2005, sequence version 2.
DT 07-MAR-2006, entry version 12.
DE Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
DE (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-
DE phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-
DE amidotransferase) (Glucosamine-6-phosphate synthase).
GN Names: glns; OrderedLocusNames=SPA3700;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OC NCBI_TaxID=54388;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 9150 / SARB42;
RX PubMed=15531882; DOI=10.1038/ngl470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozerky P., McJellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
RA Delehaanty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Sleeth J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274(2004).
CC -!- FUNCTION: Catalyzes the first step in hexosamine metabolism,
CC converting fructose-6P into glucosamine-6P using glutamine as a
CC nitrogen source (By similarity).
CC -!- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-
CC glutamate + D-glucosamine 6-phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC -!- SIMILARITY: In the C-terminal section; belongs to the SIS family.
CC -!- GFAT subfamily.
CC -!- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; CP000026; AAV79492.1; -; Genomic_DNA.
CC SMR; Q5PKV9; 1-239, 243-608.
CC GenomeReviews; CP000026_GR; SPA3700.
CC HAMAP; MF 00164; -.
CC InterPro; IPR000583; GATase.2.
CC InterPro; IPR005855; GlnS_trans.
CC InterPro; IPR001347; SIS.
CC Pfam; PF00310; GATase_2; 1.
CC Pfam; PF01380; SIS; 2.
CC TIGRFAMs; TIGR01135; glns; 1.
CC PROSITE; PS00443; GATASE_TYPE_II; 1.
KW Amino transferase; Complete proteome; Glutamine amidotransferase;
KW Transferase.
FT INIT_MET 0 0 By similarity.
FT CHAIN 1 608 Glucosamine--fructose-6-phosphate
FT aminotransferase [isomerizing].
FT FTID=PRO 0000135373.
FT REGION 1 240 Glutamine amidotransferase.
FT ACT_SITE 1 1 GATase (By similarity).
FT ACT_SITE 603 Isomerization Fru-6P (By similarity).
SQ SEQUENCE 608 AA; 66719 MW; EE20C7F1996B742B CRC64;

Query Match 99.1%; Score 3058; DB 1; Length 608;
Best Local Similarity 99.2%; Pred. No. 1.6e-184;
Matches 603; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 CGIVGAIAQRDVAAEILLEGRLRLRYGYDSAGLAVVDAEGHMTLRRLKGVQMLAQAAEE 61
DB 1 CGIVGAIAQRDVAAEILLEGRLRLRYGYDSAGLAVVDAEGHMTLRRLKGVQMLAQAAEE 60
QY 62 HPLHGCGTGAHTRWATHGEPSEVNAHPVSEHIVVHNGIENHPELREELKARGYTFVS 121
DB 61 HPLHGCGTGAHTRWATHGEPSEVNAHPVSEHIVVHNGIENHPELREELKARGYTFVS 120

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QY 122 ETDTEVIAHLVNWELKOGGTLREAVLRAIPQLRGAYGTVMDSRHPDPTLLAARSGSPLVI 181
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QY 182 GLGNGENFIASDQALLPVTRRFIFLEEGDIAETIRSVNIPDKTGAEVKRDIESNLQY 241
DB 181 GLGNGENFIASDQALLPVTRRFIFLEEGDIAETIRSVNIPDKTGAEVKRDIESNLQY 240
QY 242 DAGDKGIYRHYMQKEIYEQNAIKNTLTGRISHGQVDLSLSELGNADDELLSKVHEIQILAC 301
DB 241 DAGDKGIYRHYMQKEIYEQNAIKNTLTGRISHGQVDLSLSELGNADDELLSKVHEIQILAC 300
QY 302 GTSYNSGMVSRYPFESLAGIPCDVEIASPEYRKSAVRNLSLMTLSQSGETADTLAQLR 361
DB 301 GTSYNSGMVSRYPFESLAGIPCDVEIASPEYRKSAVRNLSLMTLSQSGETADTLAQLR 360
QY 362 LSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLTVLLMLVAKLS 421
DB 361 LSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLTVLLMLVAKLS 420
QY 422 RLKGLDASIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEEDFSKXHALFLGRGDQYPIAL 481
DB 421 RLKGLDASIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEEDFSKXHALFLGRGDQYPIAL 480
QY 482 EGALKLKEISYIIHAEYAAAGELKHGFLALIDAMPVIVVAPNNELLEKLKSNIEEVRAR 541
DB 481 EGALKLKEISYIIHAEYAAAGELKHGFLALIDAMPVIVVAPNNELLEKLKSNIEEVRAR 540
QY 542 GQLYVFADQDAGFVSSDNMHIIEMPHVEEVIAPFYTVPQLLAYHVALIKGTDVDDQPN 601
DB 541 GQLYVFADQDAGFVSSDNMHIIEMPHVEEVIAPFYTVPQLLAYHVALIKGTDVDDQPN 600
QY 602 LAKSVTVE 609
DB 601 LAKSVTVE 608

RESULT 10
Q57HY2_SALCH PRELIMINARY; PRT; 609 AA.
AC Q57HY2;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE L-glutamine:D-fructose-6-phosphate aminotransferase.
GN Name=glms; OrderedLocusNames=SC3774; ORFNames=SC3774;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=591;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-867;
RX PubMed=15781495; DOI=10.1093/nar/gki297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
RA Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
RL highly invasive and resistant zoonotic pathogen.";
RL Nucleic Acids Res. 33:1690-1698(2005).
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
CC EMBL; A5017220; AAX67680.1; -; Genomic_DNA.
DR SNR; Q57HY2; 2-240, 244-609.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0004360; F:glutamine-fructose-6-phosphate transaminase. . .; IEA.
DR GO; GO:0005529; F:sugar binding; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0016051; P:carbohydrate biosynthesis; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000583; GATase_2.
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DR InterPro; IPR005955; GLms_trans.
DR InterPro; IPR001347; SIS.
DR Pfam; PF00310; GATase_2; 1.
DR Pfam; PF01380; SIS; 2.
DR TIGRFAMs; TIGR01135; glms; 1.
DR PROSITE; PS00443; GATASE TYPE II; UNKNOWN 1.
KW Aminotransferase; Complete proteome; Transferase.
SQ SEQUENCE 609 AA; 66849 MW; EIDLFF6FIAPF35F5C CRC64;

Query Match
Best Local Similarity 99.1%; Score 3058; DB 2; Length 609;
Matches 602; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MCGIVGATAORDVABILLLEGRLREYRGYDSAGLAVDAEGHMTLRRLKGVQMLAQAAE 60
DB 1 MCGIVGATAORDVABILLLEGRLREYRGYDSAGLAVDAEGHMTLRRLKGVQMLAQAAE 60
QY 61 EHPHGGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHPELREELKARGYTFV 120
DB 61 EHPHGGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHPELREELKARGYTFV 120
QY 121 SETDTEVIAHLVNWELKOGGTLREAVLRAIPQLRGAYGTVMDSRHPDPTLLAARSGSPLV 180
DB 121 SETDTEVIAHLVNWELKOGGTLREAVLRAIPQLRGAYGTVMDSRHPDPTLLAARSGSPLV 180
QY 181 IGLNGENFIASDQALLPVTRRFIFLEEGDIAETIRSVNIPDKTGAEVKRDIESNLQ 240
DB 181 IGLNGENFIASDQALLPVTRRFIFLEEGDIAETIRSVNIPDKTGAEVKRDIESNLQ 240
QY 241 YDAGDKGIYRHYMQKEIYEQNAIKNTLTGRISHGQVDLSLSELGNADDELLSKVHEIQILA 300
DB 241 YDAGDKGIYRHYMQKEIYEQNAIKNTLTGRISHGQVDLSLSELGNADDELLSKVHEIQILA 300
QY 301 CGTSYNSGMVSRYPFESLAGIPCDVEIASPEYRKSAVRNLSLMTLSQSGETADTLAQL 360
DB 301 CGTSYNSGMVSRYPFESLAGIPCDVEIASPEYRKSAVRNLSLMTLSQSGETADTLAQL 360
QY 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLTVLLMLVAKL 420
DB 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLTVLLMLVAKL 420
QY 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEEDFSKXHALFLGRGDQYPIA 480
DB 421 ARLKGLDTSIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEEDFSKXHALFLGRGDQYPIA 480
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DB 481 LEGALKLKEISYIIHAEYAAAGELKHGFLALIDAMPVIVVAPNNELLEKLKSNIEEVRAR 540
QY 541 GGQLYVFADQDAGFVSSDNMHIIEMPHVEEVIAPFYTVPQLLAYHVALIKGTDVDDQPR 600
DB 541 GGQLYVFADQDAGFVSSDNMHIIEMPHVEEVIAPFYTVPQLLAYHVALIKGTDVDDQPR 600
QY 601 NLAKSVTVE 609
DB 601 NLAKSVTVE 609

RESULT 11
GLMS_SALTY
ID GLMS_SALTY STANDARD; PRT; 608 AA.
AC Q8ZKX1;
DT 11-JUL-2002, integrated into UniProtKB/Swiss-Prot.
DT 07-MAR-2006, entry version 21.
DE Glucosamine-6-phosphate aminotransferase [isomerizing]
DE (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-
DE phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate
DE amidotransferase) (Glucosamine-6-phosphate synthase).
GN Name=glms; OrderedLocusNames=STM3861;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
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NCBI_TaxID=602;
 [1]
 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 STPAIN-LT2 / SCSC1412 / ATCC 700720; DOI=10.1038/35101614;
 MEDLINE=21534948; PubMed=11677608; DOI=10.1038/35101614;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 RT LT2.";
 RL Nature 413:852-856(2001).
 CC -1- FUNCTION: Catalyzes the first step in hexosamine metabolism,
 CC converting fructose-6P into glucosamine-6P using glutamine as a
 CC nitrogen source (By similarity).
 CC -1- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-
 CC glutamate + D-glucosamine 6-phosphate.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
 CC -1- SIMILARITY: In the C-terminal section; belongs to the SIS family.
 CC GPAT subfamily.
 CC -1- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
 CC
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 CC
 CC -----
 DR ENBL; AE008880; AAU22719.1; -; Genomic_DNA.
 DR HSSP; P17169; IUXA.
 DR SMR; Q82KX1; 1-239, 243-608.
 DR GenomeReviews; AE006468 GR; STM3861.
 DR StyGene; SG7777?; glms.
 DR BioCyc; STY999287:STM3861-MONOMER; -.
 DR HAMAP; MF_00164; -; 1.
 DR InterPro; IPR000583; GATase_2.
 DR InterPro; IPR005855; Glms_trans.
 DR InterPro; IPR001347; SIS.
 DR Pfam; PF00310; GATase_2; 1.
 DR Pfam; PF01380; SIS; 2.
 DR TIGRFAMs; TIGR01135; glms; 1.
 DR PROSITE; PS00443; GATASE_TYPE_II; 1.
 KW Amidotransferase; Complete proteome; Glutamine amidotransferase;
 KW Transferase.
 FT INIT MET 0 0 By similarity.
 FT CHAIN 1 608 Glucosamine--fructose-6-phosphate
 FT /Frid=PRO.0000135375.
 FT REGION 1 240 Glutamine amidotransferase.
 FT ACT_SITE 1 1 GATase (By similarity).
 FT ACT_SITE 603 603 Isomerization Fru-6P (By similarity).
 SQ SEQUENCE 608 AA; 66746 MW; C320C7F18DEDAF52 CRC64;
 Query Match 99.0%; Score 3055; DB 1; Length 608;
 Best Local Similarity 99.0%; Pred. No. 2.5e-184;
 Matches 602; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 CGIVGATAQRDVAEILLEGRLRLRYRGYDSAGLAVDAEGHMTLRRLGKGVQLAAQAE 61
 DB 1 CGIVGATAQRDVAEILLEGRLRLRYRGYDSAGLAVDAEGHMTLRRLGKGVQLAAQAE 60
 QY 62 HPLHGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHNEPRLREELKARGYTFVS 121
 DB 61 HPLHGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHNEPRLREELKARGYTFVS 120
 QY 122 ETDTEVIAHLVNNELKQGGTLREAVLRAIPQLRGAYGTIVIMDSRHPDTLLAARSGSLVI 181
 DB 121 ETDTEVIAHLVNNELKQGGTLREAVLRAIPQLRGAYGTIVIMDSRHPDTLLAARSGSLVI 180
 QY 182 GLGNGENFIASDQALLPVTTRRFFIFLEGDIAETTRSVNIPDKTGAEVKQDIESNLQY 241
 DB 181 GLGNGENFIASDQALLPVTTRRFFIFLEGDIAETTRSVNIPDKTGAEVKQDIESNLQY 240
 QY 242 DAGDKGIYRHYMQEIIYEQPNAIKNTLTGRISHQGVDSLSELGPNADLLSKVEHIQILAC 301

DB 241 DAGDKGIYRHYMQEIIYEQPNAIKNTLTGRISHQGVDSLSELGPNADLLSKVEHIQILAC 300
 QY 302 GTSYNSGMVSRYYWFESLAGIPCDVEIASERYKSAVRNLSMTITLSQSGETADTLAQLR 361
 DB 301 GTSYNSGMVSRYYWFESLAGIPCDVEIASERYKSAVRNLSMTITLSQSGETADTLAQLR 360
 QY 362 LSKELGYLGSLAICNVPSSSLVRESDLALMTNAGTEIGVASTKRAFTTQLTVLLMLVAKLS 421
 DB 361 LSKELGYLGSLAICNVPSSSLVRESDLALMTNAGTEIGVASTKRAFTTQLTVLLMLVAKLS 420
 QY 422 RLKGLDASIEHDIHVGLQALPSRIEQMLSQDKRIEALAEFSDKHAFIFLGRGQOYPAL 481
 DB 421 RLKGLDASIEHDIHVGLQALPSRIEQMLSQDKRIEALAEFSDKHAFIFLGRGQOYPAL 480
 QY 482 EGALKLKEISYIHAAYAGELKHGPLALIDAMPVIVVAPNNELLEKLSNIEEVRARG 541
 DB 481 EGALKLKEISYIHAAYAGELKHGPLALIDAMPVIVVAPNNELLEKLSNIEEVRARG 540
 QY 542 GOLYVFADQDAGFVSSDNMHIIEMPHVEEVIAPITFYTPVPLQLLAYHVALIKGTDVDDPRN 601
 DB 541 GOLYVFADQDAGFVSSDNMHIIEMPHVEEVIAPITFYTPVPLQLLAYHVALIKGTDVDDPRN 600
 QY 602 LAKSVTVE 609
 DB 601 LAKSVTVE 608
 RESULT 12
 GLMS_SALTI
 ID _GLMS_SALTI STANDARD; PRT; 608 AA.
 AC Q8Z202;
 DT 11-JUL-2002, integrated into UniProtKB/Swiss-Prot.
 DT 11-JUL-2002, sequence version 2.
 DT 07-MAR-2006, entry version 27.
 DE Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
 DE (SC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-
 DE phosphate amidotransferase) (GPAT) (L-glutamine-D-fructose-6-phosphate
 DE amidotransferase) (Glucosamine-6-phosphate synthase).
 GN Name:glms; OrderedLocusNames=STY3917, t3658;
 OS *Salmonella typhi*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Salmonella*.
 OX NCBI_TaxID=601;
 [1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=CT18;
 RC MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT enterica serovar typhi CT18.";
 RL Nature 413:848-852(2001).
 [2]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RP STRAIN=Ty2 / ATCC 700931;
 RC MEDLINE=22531367; PubMed=12644504;
 RX DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodyanovski V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of *Salmonella enterica* serovar Typhi strains Ty2
 RT and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 CC -1- FUNCTION: Catalyzes the first step in hexosamine metabolism,
 CC converting fructose-6P into glucosamine-6P using glutamine as a
 CC nitrogen source (By similarity).
 CC -1- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-


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FT REGION 1 241 Glutamine amidotransferase.
FT ACT_SITE 1 1 GATase (By similarity).
FT ACT_SITE 604 604 Isomerization Fru-6P (By similarity).
SQ SEQUENCE 609 AA; 6686 MW; BFE71B8EDFD23B5D CRC64;

Query Match 36.9%; Score 2681.5; DB 1; Length 609;
Best Local Similarity 85.1%; Pred. No. 1e-160;
Matches 518; Conservative 46; Mismatches 44; Indels 1; Gaps 1;

QY 2 CGIVGATQDVAEILLEGRLLECYGYDSAGLAVDAEGHMTLRRLRGKQVQLAQAAE 61
Db 1 CGIVGAVAQDVAEILLEGRLLECYGYDSAGLAVDSEGHVARLRRLRGKQVLSQAAE 60
QY 62 HPLHGGTGIAHTRWATGEPSEVNAHPVSEHIVVHNGIIEHPEELKARGTYFVS 121
Db 61 HELHGGTGIAHTRWATGEPSEENAHPHISEHITIVHNGIIEHPELRMLIGRGYFVS 120
QY 122 ETDETVAHVLNNELKQ-GGTLREAVLRAIPQURGAYGTVMDSRHPDTLAARSGLV 180
Db 121 ETDETVAHVLHVEFEQKQGGTLVEVVKRVIPQLRGAYGMVLDNRDSSVLVAARSGPLV 180
QY 181 IGLGMENFTASDQALLPYTRRFIFLEEGDIAEITRSYNIIFDKTCAEVKRODIESNLQ 240
Db 181 IGRGVGENFTASDQALLPYTRRFMFLEEGDVAEITRDVRFVDFKSGQLATREEIESKVS 240
QY 241 YDAGDKGIYRHYMQEYIOPNAIKNTLTGRISHGOVDLSELGPNADLLSKVHEHIQILA 300
Db 241 YDAGDKGAYRHYMQEYIOPMAIKNTLEGRFSHGEINLSELGPKADELLAKVHEVQIIA 300
QY 301 CGTSYNGMVSRVYFESLAGIPCDVEITASEFRYKRSVNRNSLMTLSQSGETADTLA 360
Db 301 CGTSYNGMVSRVYFEEALGIPCDVEITASEFRYKRPVNRNSLMTLSQSGETADTLAAL 360
QY 361 RLSEKELGSLGSLAICNVPGSSLVRESLALMTWAGTEIGVASTKAFPTQLTVLLMLVAKL 420
Db 361 RLSEKELGSLGSLAICNVAGSSLVRESDMALMTKAGVEIGVASTKAFPTQLTVLLMLVARV 420
QY 421 SRLKGLDASLEHDIHVGLQALPSRIEOMLSQDKRIEALAEFDKXHALFLGRGDQVPIA 480
Db 421 GLRUGMDAQIEHDIHVGLQALPARIEQMLSQDKLIESLAGFSDKXHALFLGRGDQVPIA 480
QY 481 LEGALKLKEISYTHAEYAAAGELKHGPLALIDADMPVIVVAPNNLEKLKSNIEEVRAR 540
Db 481 MEGALKLKEISYTHAEYAAAGELKHGPLALIDADMPVVVAPNNLEKLKSNIEEVRAR 540
QY 541 CGQLYVPADQAGFVSDNNHIIEMPHVESVIARIFVTVPQLLAYHVALIKGTVDVQPR 600
Db 541 GGLYVFADEDAGFTSENKKIIPLPHIEEVIARIFVTVPQLLQSLYHVALIKGTVDVQPR 600
QY 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 14
GLMS_YERPE
ID_GLMS_YERPE STANDARD; PRT; 608 AA.
AC Q82958;
DT 11-JUL-2002, integrated into UniProtKB/Swiss-Prot.
DT 11-JUL-2002, sequence version 2.
DT 07-MAR-2006, entry version 32.
DE Glucoseamine--fructose-6-phosphate aminotransferase [isomerizing]
DE (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate
DE phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate
DE amidotransferase) (Glucoseamine-6-phosphate synthase).
GN Name=glms; OrderedLocusNames=YPO4118, Y4132, YP4025;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
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RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdono-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feitwell T., Hamlin N., Holtroyd S., Jagers K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KIMS / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Liss P.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15368893; DOI=10.1093/dnares/11.3.179;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT avirulent to humans.";
RL DNA Res. 11:179-197(2004).
CC -I- FUNCTION: Catalyzes the first step in hexosamine metabolism,
CC converting fructose-6P into glucosamine-6P using glutamine as a
CC nitrogen source (By similarity).
CC -I- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-
CC glutamate + D-glucosamine 6-phosphate.
CC -I- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC -I- SIMILARITY: In the C-terminal section; belongs to the SIS family.
CC GFAT subfamily.
CC -I- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
CC -----
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CC -----
CC ENBL; AJ414160; CAC93567.1; -; Genomic_DNA.
CC ENBL; AE014014; AAM87674.1; -; Genomic_DNA.
CC ENBL; AE017142; AAS64164.1; -; Genomic_DNA.
CC PIR; AB0500; AB0500.
CC HSSP; P17169; 1MOS.
CC SNR; Q82958; 1-239, 243-608.
CC GenomeReviews; AE009952_GK; Y4132.
CC GenomeReviews; AE017042_GK; YP4025.
CC GenomeReviews; AL590842_GK; YPO4118.
CC BioCyc; YPES187410.Y4132-MONOMER; -.
CC BioCyc; YPES632.YPO4118-MONOMER; -.
CC HAMAP; MF_00164; -.
CC InterPro; IPR000583; GATase_2.
CC InterPro; IPR005855; Glms_trans.
CC InterPro; IPR001347; SIS.
CC Pfam; PF00310; GATase_2; 1.
CC TIGRFAMs; TIGR01135; glms; 1.
CC PROSITE; PS00443; GATASE_TYPE_II; 1.
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FT /FTID=PRO_0000135418.
FT REGION 1 240 Glutamine amidotransferase.
FT ACT_SITE 1 1 GATase (By similarity).
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FT ACT SITE 603 603 Isomerization Fru-6P (By similarity).
SQ SEQUENCE 608 AA; 66394 MW; 1655FD0ADB16CCD6 CRC64;

Query Match
Best Local Similarity 86.7%; Score 2677; DB 1; Length 608;
Matches 517; Conservative 44; Mismatches 47; Indels 0; Gaps 0;

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Db 181 GCGVGENFIASDQALLPVTTRRFFLEEGDVVEVTRRSISIFDKQNAIERPEIESQVQY 240

QY 182 GLGNGENFIASDQALLPVTTRRFFLEEGDIAETRRSVNIIFDKTGAEVKRDIESNLO 241
Db 181 GCGVGENFIASDQALLPVTTRRFFLEEGDVVEVTRRSISIFDKQNAIERPEIESQVQY 240

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AC O663R1;
DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
DT 30-AUG-2005, sequence version 2.
DT 30-AUG-2006, entry version 16.
DE Glucosamine-6-phosphate aminotransferase (isomerizing)
DE (EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-
DE phosphate amidotransferase) (GPA) (L-glutamine-D-fructose-6-phosphate
DE amidotransferase) (Glucosamine-6-phosphate synthase).
GN Names:glms; OrderedLocusNames=YPTB3964;
OS Versinia pseudotuberculosis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype I;
RC PubMed=1538856; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
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RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Versinia pseudotuberculosis ";
RT comparison with Versinia pseudotuberculosis ";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -!- FUNCTION: Catalyzes the first step in hexosamine metabolism,
CC converting fructose-6P into glucosamine-6P using glutamine as a
CC nitrogen source (By similarity).
CC -!- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-
CC glutamate + D-glucosamine 6-phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC -!- SIMILARITY: In the C-terminal section; belongs to the SIS family.
CC GFAT subfamily.
CC -!- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
CC -----
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CC -----
CC EMBL; BX936398; CAH23202.1; -; Genomic_DNA.
CC SMR; Q663R1; 1-239, 243-608.
CC GenomeReviews; BX936398 GR; YPTB3964.
CC HAMAP; MF_00164; -; 1.
CC InterPro; IPR000583; GATase_2.
CC InterPro; IPR005855; GlnS_trans.
CC InterPro; IPR001347; SIS.
CC Pfam; PF00310; GATase_2; 1.
CC TIGRFAMs; TIGR01135; glms; 1.
CC PROSITE; PS00443; GATASE_TYPE_II; 1.
CC Aminotransferase; Complete proteome; Glutamine amidotransferase;
CC Transferrase.
FT INIT MET 0 0 By similarity.
FT CHAIN 1 608 Glucosamine-6-phosphate
FT aminotransferase [isomerizing].
FT /FTID=PRO_0000135419
FT REGION 1 240 Glutamine amidotransferase.
FT ACT_SITE 1 1 GATase (By similarity).
FT ACT_SITE 603 603 Isomerization Fru-6P (By similarity).
SQ SEQUENCE 608 AA; 66394 MW; 1655FD0ADB16CCD6 CRC64;

Query Match
Best Local Similarity 86.7%; Score 2677; DB 1; Length 608;
Matches 517; Conservative 44; Mismatches 47; Indels 0; Gaps 0;

QY 2 CGIVGAIQAQRDVAEILLEGRLRLEIRYGYDSAGLAVVDAGHMTLRRLGKVMQLAAAE 61
Db 1 CGIVGVAQORDIAEILLEGRLRLEIRYGYDSAGLAVVDSEGLTFLRRVGVKHALSDAAEK 60

QY 62 HPLGGTGTIAHTRWATHGEPSEANAPHVSEHIVVHNGIENHEPRLREELKARGTYFVS 121
Db 61 QDLGGTGTIAHTRWATHGEPSEANAPHVSDYISVHNGIENHEPRLREELISRGYRFS 120

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Db 121 ETDTEVIAHLVHVEQOQGSLLVVKRVIPLQRCAYGTVVWDSRDLRAARSGSLVI 180

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Db 181 GCGVGENFIASDQALLPVTTRRFFLEEGDVVEVTRRSISIFDKQNAIERPEIESQVQY 240

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QY 362 LSKELGYLGLSLAICNVAGSSLVRESLALMTNAGTIGVASTKFTQTLTLLMLVAKLS 421
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Db	481	EGALKLKEISYI	HAEAYAAGELKHG	PLALIDADMP	VI	VVAPNNELLEKLKS	NIEEVRARG 540
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Qy	602	LAKSVTVE	609				
Db	601	LAKSVTVE	608				

Search completed: August 7, 2006, 09:24:37
Job time : 157 secs

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OM protein - protein search, using sw model

Run on: August 7, 2006, 09:25:52 ; Search time 24 Seconds
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Title: US-10-612-779-2

Perfect score: 3086

Sequence: 1 MCGIVGAIQRDVAEILLEG.....LIRGTDVDPNRLAKSVTVE 609

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /EMC_Celerra_SID33/ptodata/2/iaa/6_COMB.pep.*
- 3: /EMC_Celerra_SID33/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC_Celerra_SID33/ptodata/2/iaa/H_COMB.pep.*
- 5: /EMC_Celerra_SID33/ptodata/2/iaa/PTCUT_COMB.pep.*
- 6: /EMC_Celerra_SID33/ptodata/2/iaa/RE_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3086	100.0	609	2	US-09-115-475-16
2	3080	99.8	609	2	US-09-115-475-28
3	3080	99.8	609	2	US-09-115-475-31
4	3079	99.8	609	2	US-09-115-475-25
5	3071	99.5	609	2	US-09-115-475-19
6	3068	99.4	609	2	US-09-115-475-22
7	2876	93.2	651	2	US-09-489-039A-10691
8	2510.5	81.4	622	2	US-09-543-681A-7522
9	1995	64.6	616	2	US-09-252-991A-19164
10	1780.5	57.7	613	2	US-09-328-352-5065
11	1492.5	48.4	619	2	US-09-540-236-2182
12	1362.5	44.2	572	2	US-09-902-540-16012
13	1357.5	44.0	592	1	US-08-599-171A-30
14	1357.5	44.0	592	1	US-08-646-590B-30
15	1357.5	44.0	592	2	US-09-069-226-30
16	1357.5	44.0	592	2	US-09-412-184-30
17	1155	37.4	611	2	US-09-438-185A-970
18	1137	36.8	655	2	US-09-107-532A-4425
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21	1115	36.2	619	2	US-09-134-001C-4248
22	1103.5	35.8	682	1	US-08-911-445-3
23	1103.5	35.8	682	2	US-09-182-983-3
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25	1103.5	35.8	682	2	US-09-949-016-6591
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27	960.5	31.1	615	1	US-08-911-445-2	Sequence 2, Appli
28	960.5	31.1	615	2	US-09-182-983-2	Sequence 2, Appli
29	960.5	31.1	615	2	US-09-771-838A-2	Sequence 2, Appli
30	846.5	27.4	640	2	US-09-134-000C-3871	Sequence 3871, Ap
31	745	24.1	487	2	US-09-248-796A-17250	Sequence 17250, A
32	704	22.8	365	2	US-09-549-016-11214	Sequence 11214, A
33	677	21.9	405	2	US-09-710-279-232	Sequence 232, App
34	612.5	19.8	422	2	US-09-270-767-45187	Sequence 45187, A
35	574	18.6	486	1	US-08-911-445-18	Sequence 18, Appl
36	574	18.6	486	2	US-09-182-983-18	Sequence 18, Appl
37	574	18.6	486	2	US-09-771-838A-18	Sequence 18, Appl
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39	573	18.6	425	2	US-09-182-983-1	Sequence 1, Appli
40	573	18.6	425	2	US-09-771-838A-1	Sequence 320, App
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42	496	16.1	307	2	US-09-198-452A-1041	Sequence 1040, Ap
43	360.5	11.7	161	2	US-09-198-452A-1040	Sequence 18074, A
44	332	10.8	708	2	US-09-252-991A-18074	Sequence 18074, A
45	320	10.4	182	2	US-09-198-452A-1042	Sequence 1042, Ap

ALIGNMENTS

RESULT 1

US-09-115-475-16

; Sequence 16, Application US/09115475

; Patent No. 6372457

; GENERAL INFORMATION:

; APPLICANT: Betty, Alan

; APPLICANT: Burlingame, Richard P.

; APPLICANT: Millis, James R.

; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE

; FILE REFERENCE: 3161-18-C1

; CURRENT APPLICATION NUMBER: US/09/115,475

; CURRENT FILING DATE: 1998-07-15

; EARLIER APPLICATION NUMBER: PCT/US98/00800

; EARLIER FILING DATE: 1998-01-14

; EARLIER APPLICATION NUMBER: 60/035,494

; EARLIER FILING DATE: 1997-01-14

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 16

; LENGTH: 609

; TYPE: PRT

; ORGANISM: Escherichia coli

US-09-115-475-16

Query Match 100.0%; Score 3086; DB 2; Length 609;
Best Local Similarity 100.0%; Pred. No. 3.7e-295;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	181	IGLGMENFIASQDALLPVTRRFIFLEGGDIAEITRRSVNIFDKTGAEVKRDIESNLQ 240	Sequence 18, Appl
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Db 601 NLAKSVTVE 609
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RESULT 2

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US-09-115-475-28
; Sequence 28, Application US/09115475
; Patent No. 6372457
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/09/115,475
; CURRENT FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: PCT/US98/00800
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,494
; EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-115-475-28
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Best Local Similarity 99.8%; Pred. No. 1.5e-294;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 61 EHPHGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHPELREELKARGYTFV 120
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RESULT 3
US-09-115-475-31
; Sequence 31, Application US/09115475
; Patent No. 6372457
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/09/115,475
; CURRENT FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: PCT/US98/00800
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,494
; EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
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; SEQ ID NO 31
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-115-475-31
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Query Match 99.8%; Score 3080; DB 2; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.5e-294;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIAQRDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRLKGVMQAQAAE 60
Db 1 MCGIVGAIAQRDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRLKGVMQAQAAE 60
Qy 61 EHPHGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHPELREELKARGYTFV 120
Db 61 EHPHGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHPELREELKARGYTFV 120
Qy 121 SETDTEVIAHLVNMWELKQGGLTREAIVLRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNMWELKQGGLTREAIVLRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Qy 181 IGLGMGENFIASDQALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRDIESNLQ 240
Db 181 IGLGMGENFIASDQALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRDIESNLQ 240
Qy 241 YDAGDKGIYRHYMKEIYEOPNAIKNTLTGRI SHGQVDLSLGNADLELLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMKEIYEOPNAIKNTLTGRI SHGQVDLSLGNADLELLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRWYFESLAGIPCDVEIASFEFRYKSAVRNSLMTLSQSGETADTLA 360
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Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFRYKSAVRNSLMIITLSQGETADTTLA 360
Qy 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQTLTVLLMLVAKL 420
Db 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQTLTVLLMLVAKL 420
Qy 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEDFSDKHHALFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEDFSDKHHALFLSRGDQYPIA 480
Qy 481 LEGALKLKEISYTHAEAYAAAGELKHGPLALIDADMPVIVVAPNNELLEKLKSNIEEVRAR 540
Db 481 LEGALKLKEISYTHAEAYAAAGELKHGPLALIDADMPVIVVAPNNELLEKLKSNIEEVRAR 540
Qy 541 GGQLYVPADQAGFVSSDNHIIEMPHVEEVIAPIFYTVPLQLLAYHVALIKGTDVQDPR 600
Db 541 GGQLYVPADQAGFVSSDNHIIEMPHVEEVIAPIFYTVPLQLLAYHVALIKGTDVQDPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609
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RESULT 4
US-09-115-475-25
; Sequence 25, Application US/09115475
; Patent No. 6372457
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/09/115,475
; CURRENT FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: PCT/US98/00800
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,494
; EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-115-475-25
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Query Match 99.8%; Score 3079; DB 2; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.8e-294;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIAQORDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRLGKVQMLAQAAE 60
Db 1 MCGIVGAIAQORDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRLGKVQMLAQAAE 60

Qy 61 EPHLHGCTGTAHTRWATHGEPSEVNAHPHVSSEHIVVHNGIIEHNEPLRELKARGYTFV 120
Db 61 EPHLHGCTGTAHTRWATHGEPSEVNAHPHVSSEHIVVHNGIIEHNEPLRELKARGYTFV 120

Qy 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPLV 180

Qy 181 IGLGMGFNIASDQALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRDIESNLQ 240
Db 181 IGLGMGFNIASDQALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRDIESNLQ 240

Qy 241 YDAGDKGIYRHYMKEIYEOPNAIKNTLTGRISHGQVDLSLGNADLLSKVSHIQILA 300
Db 241 YDAGDKGIYRHYMKEIYEOPNAIKNTLTGRISHGQVDLSLGNADLLSKVSHIQILA 300

Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFRYKSAVRNSLMIITLSQGETADTTLA 360
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Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFRYKSAVRNSLMIITLSQGETADTTLA 360
Qy 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQTLTVLLMLVAKL 420
Db 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQTLTVLLMLVAKL 420
Qy 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEDFSDKHHALFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEDFSDKHHAPFLGRGDQYPIA 480
Qy 481 LEGALKLKEISYTHAEAYAAAGELKHGPLALIDADMPVIVVAPNNELLEKLKSNIEEVRAR 540
Db 481 LEGALKLKEISYTHAEAYAAAGELKHGPLALIDADMPVIVVAPNNELLEKLKSNIEEVRAR 540
Qy 541 GGQLYVPADQAGFVSSDNHIIEMPHVEEVIAPIFYTVPLQLLAYHVALIKGTDVQDPR 600
Db 541 GGQLYVPADQAGFVSSDNHIIEMPHVEEVIAPIFYTVPLQLLAYHVALIKGTDVQDPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609
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RESULT 5
US-09-115-475-19
; Sequence 19, Application US/09115475
; Patent No. 6372457
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/09/115,475
; CURRENT FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: PCT/US98/00800
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,494
; EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-115-475-19
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Query Match 99.5%; Score 3071; DB 2; Length 609;
Best Local Similarity 99.5%; Pred. No. 1.1e-293;
Matches 606; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MCGIVGAIAQORDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRLGKVQMLAQAAE 60
Db 1 MCGIVGAIAQORDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRLGKVQMLAQAAE 60

Qy 61 EPHLHGCTGTAHTRWATHGEPSEVNAHPHVSSEHIVVHNGIIEHNEPLRELKARGYTFV 120
Db 61 EPHLHGCTGTAHTRWATHGEPSEVNAHPHVSSEHIVVHNGIIEHNEPLRELKARGYTFV 120

Qy 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPLV 180

Qy 181 IGLGMGFNIASDQALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRDIESNLQ 240
Db 181 IGLGMGFNIASDQALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRDIESNLQ 240

Qy 241 YDAGDKGIYRHYMKEIYEOPNAIKNTLTGRISHGQVDLSLGNADLLSKVSHIQILA 300
Db 241 YDAGDKGIYRHYMKEIYEOPNAIKNTLTGRISHGQVDLSLGNADLLSKVSHIQILA 300

Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFRYKSAVRNSLMIITLSQGETADTTLA 360
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Db 301 CGTSYNSGMVSRWYFESLAGIPCDVEIASSEFRYKSAVRNSLMTLSQSGETADTLAGL 360
QY 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLTVLLMLVAKL 420
Db 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLTVLLMLVAKL 420
QY 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSQDKRIEALAEFSDKHHLFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSQDKRIEALAEFSDKHHLFLGRGDQYPIA 480
QY 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
Db 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
QY 541 GGQLYVFADQDAGFVSSDDNMHIIEMPHVEEVIAPFYTVPLQLLAYHVALIKGTDVQDPR 600
Db 541 GGQLYVFADQDAGFVSSDDNMHIIEMPHVEEVIAPFYTVPLQLLAYHVALIKGTDVQDPR 600
QY 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 6

US-09-115-475-22
; Sequence 22, Application US/09115475
; Patent No. 6372457
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/09/115,475
; CURRENT FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: PCT/US98/00800
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,494
; EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-115-475-22

Query Match 99.4%; Score 3068; DB 2; Length 609;
Best Local Similarity 99.5%; Pred. No. 2.2e-293;
Matches 606; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MCGIVGAIAORDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRRLRGKQVQLAAQAAE 60
Db 1 MCGIVGAIAORDVAEILLEGRLRLEYRGYDSAGLAVVDEGHMTLRRLRGKQVQLAAQAAE 60
QY 61 EPHLHGTTGTAHTRWATHGEPSEVNAHPHVSHEHVVVHNGIIEHNEPLREELKARGYTFV 120
Db 61 EPHLHGTTGTAHTRWATHGEPSEVNAHPHVSHEHVVVHNGIIEHNEPLREELKARGYTFV 120
QY 121 SETDTEVIAHLVNWELKQGTLREAVLRAIPQLRGAYGTVMDSRHPDPTLLAARSGSPVL 180
Db 121 SETDTEVIAHLVNWELKQGTLREAVLRAIPQLRGAYGTVMDSRHPDPTLLAARSGSPVL 180
QY 181 IGLGMENFIASDQALLPVTTRRFIFLEEGDIAETRRSVNIFDKTGAEVKQDIENSLQ 240
Db 181 IGLGMENFIASDQALLPVTTRRFIFLEEGDIAETRRSVNIFDKTGAEVKQDIENSLQ 240
QY 241 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSLGNADLELSKVHIIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSLGNADLELSKVHIIQILA 300
QY 301 CGTSYNSGMVSRWYFESLAGIPCDVEIASSEFRYKSAVRNSLMTLSQSGETADTLAGL 360

Db 301 CGTSYNSGMVSRWYFESLAGIPCDVEIASSEFRYKSAVRNSLMTLSQSGETADTLAGL 360
QY 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLTVLLMLVAKL 420
Db 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLTVLLMLVAKL 420
QY 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSQDKRIEALAEFSDKHHLFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSQDKRIEALAEFSDKHHLFLGRGDQYPIA 480
QY 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
Db 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
QY 541 GGQLYVFADQDAGFVSSDDNMHIIEMPHVEEVIAPFYTVPLQLLAYHVALIKGTDVQDPR 600
Db 541 GGQLYVFADQDAGFVSSDDNMHIIEMPHVEEVIAPFYTVPLQLLAYHVALIKGTDVQDPR 600
QY 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 7

US-09-489-039A-10691
; Sequence 10691, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10691
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10691

Query Match 93.2%; Score 2876; DB 2; Length 651;
Best Local Similarity 92.1%; Pred. No. 2.2e-274;
Matches 561; Conservative 29; Mismatches 19; Indels 0; Gaps 0;

QY 1 MCGIVGAIAORDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRRLRGKQVQLAAQAAE 60
Db 43 MCGIVGAIAORDVAEILLEGRLRLEYRGYDSAGLAVVDEGHMTLRRLRGKQVQLAAQAAE 102
QY 61 EPHLHGTTGTAHTRWATHGEPSEVNAHPHVSHEHVVVHNGIIEHNEPLREELKARGYTFV 120
Db 103 EPHLHGTTGTAHTRWATHGEPSEVNAHPHVSHEHVVVHNGIIEHNEPLRALLQSRGYVVF 162
QY 121 SETDTEVIAHLVNWELKQGTLREAVLRAIPQLRGAYGTVMDSRHPDPTLLAARSGSPVL 180
Db 163 TETDTEVIAHLVHWELEQGGTLREAVLRAIPQLRGAYGTVMIDTRDPTLLAARSGSPVL 222
QY 181 IGLGMENFIASDQALLPVTTRRFIFLEEGDIAETRRSVNIFDKTGAEVKQDIENSLQ 240
Db 223 IGLGMENFIASDQALLPVTTRRFIFLEEGDIAETRRSVVIFDKSAQVVKQIESNLQ 282
QY 241 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSLGNADLELSKVHIIQILA 300
Db 283 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGEVDLSLGNADLELSKVHIIQIVA 342
QY 301 CGTSYNSGMVSRWYFESLAGIPCDVEIASSEFRYKSAVRNSLMTLSQSGETADTLAGL 360
Db 343 CGTSYNSGMVSRWYFESLAGIPCDVEIASSEFRYKSAVRNSLMTLSQSGETADTLAGL 402
QY 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLTVLLMLVAKL 420

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Db 403 RLSKELGYLSLAICNVPGSSLVRESLALMTKAGTIGVASTKFTTQLTVLLMLVAKL 462
Qy 421 SRLKGLDASIEHDI VHGLQALPSRIEOMLSQDKRIEALAEFSDKXHALFLGRGDQYPIA 480
Db 463 ARUKQDASIEHDI VHGLQALPNRIEOMLSQDKRIEALAEFSDKXHALFLGRGDQYPIA 522
Qy 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNLELEKLSNIEEVRAR 540
Db 523 MEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNLELEKLSNIEEVRAR 582
Qy 541 GGQLYVPADQADGAFVSSDNMHHIEMPHVEEVIAPIFTYVPLQLLAYHVALIKGTDVDPQR 600
Db 583 GGELYVPADGAGFNGSDNMHHIEMPHVEETIAPIFTYVPLQLLAYHVALIKGTDVDPQR 642
Qy 601 NLAKSVTVE 609
Db 643 NLAKSVTVE 651

RESULT 8
US-09-543-681A-7522
; Sequence 7522, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7522
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7522

Query Match 81.4%; Score 2510.5; DB 2; Length 622;
Best Local Similarity 81.1%; Pred. No. 2.4e-238;
Matches 494; Conservative 46; Mismatches 68; Indels 1; Gaps 1;

Qy 1 MCGIVGAIAORDVAEILLEGRLREYRGYSAGLAVVDAGHMTLRLRLGKVMQLAQAE 60
Db 15 MCGIVGAIAORDVAEILLEGRLREYRGYSAGLAVVDNDCHMTLRLREVGVQMLAEAE 74
Qy 61 EPHLHGCTGTAHTRWATHGEPSEVNAHPHYSEHIVVHNGIENHEPLRBEELKARGYTFV 120
Db 75 KTQVIGGTGTAHTRWATHGEPQDNAPHYSGTTAVVHNGIENYQELKAELINRGYQFA 134
Qy 121 SETDTEVIAHLVNWELKOGGTLREAVLRAIPQLRGAYGTVMDSRHPDPTLLAARSGSPLV 180
Db 135 SQTDTTEVIAHLVNWEOQGGLREWQVPIQLRGAYGTVMDSRTPPELLVAARSGSPLV 194
Qy 181 IGLCMGFENFASDQALLPVTRRFIFLEEGDIAETRRSVNI PKDTGAEVKRODIESNLQ 240
Db 195 VGLGVGFENFLASDQALLPVTRRFIFLEEGDIVEITRRHNYIDVNGEENRDIIESNVQ 254
Qy 241 YDAGDKGIYRHYMKEIYEQNALKNLTGTGRISHGQVDLSLGPNADELKSKVEHIQILA 300
Db 255 YDAGDKGIYRHYMKEIYEQPLAKNTLEGLKAEISDLSGLSKAPEILISOVEHIQIVA 314
Qy 301 CGTSYNGMVSRYWFESLAGIPCDVEIASFEPRYKSAVRNLSMITLSQSGETADTLAAGL 360
Db 315 CGTSYNGMVSRYWFESLAGIPCDVEIASFEPRYKSAVRNLSMITLSQSGETADTLAAL 374
Qy 361 RLSKELGYLSLAICNVPGSSLVRESLALMTNAGTIGVASTKFTTQLTVLLMLVAKL 420
Db 375 RLSKELGYLSLAICNVAGSSLVRESFVLMTKAGAEIGVASTKFTTQLAVLLMLVAYM 434
Qy 421 SRLKGLDASIEHDI VHGLQALPSRIEOMLSQDKRIEALAEFSDKXHALFLGRGDQYPIA 480
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Db 435 GRITKGVEA-LEQQVAMALHALPSRIEOMLSQDKRIEALAEFSEKSHALFLGRGDQYPIA 493
Qy 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNLELEKLSNIEEVRAR 540
Db 494 VEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNLELEKLSNIEEVRAR 553
Qy 541 GGQLYVPADQADGAFVSSDNMHHIEMPHVEEVIAPIFTYVPLQLLAYHVALIKGTDVDPQR 600
Db 554 GGLLYVPADQADGAFSEETMKLISLPHVEELIAPIFTYVPLQLLSYHVALIKGTDVDPQR 613
Qy 601 NLAKSVTVE 609
Db 614 NLAKSVTVE 622

RESULT 9
US-09-252-991A-19164
; Sequence 19164, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19164
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19164

Query Match 64.6%; Score 1995; DB 2; Length 616;
Best Local Similarity 62.7%; Pred. No. 1.7e-187;
Matches 383; Conservative 101; Mismatches 125; Indels 2; Gaps 2;

Qy 1 MCGIVGAIAORDVAEILLEGRLREYRGYSAGLAVVDAGHMTLRLRLGKVMQLAQAE 60
Db 6 MCGIVGAIAERNTPILIEGLKLEYRGYSAGVAVFDNEGRLQRCRRGVKVASLEGLA 65
Qy 61 EPHLHGCTGTAHTRWATHGEPSEVNAHPHY-SEHIVVHNGIENHEPLRBEELKARGYTF 119
Db 66 GTPLLGRLGTAHTRWATHGAPTEGNAHPHFSSDELAVVHNGIENHEPLRERLKLGVYF 125
Qy 120 VSETDTEVIAHLVNWELKOGGTLREAVLRAIPQLRGAYGTVMDSRHPDPTLLAARSGSP 179
Db 126 TSQDTEVIVHLLHHKLSQSGDUTLAKDAVKELHAYGLAVISAAQPDRIVAARSGSP 185
Qy 180 VIGLGMGFENFASDQALLPVTRRFIFLEEGDIAETRRSVNI PKDTGAEVKRODIESNL 239
Db 186 VIGLGMGFENFLASDQALRQVTDRLFVLEEGDIAETRRSDVRLWDVQNDVQRETVQYHE 245
Qy 240 QYDAGDKGIYRHYMKEIYEQNALKNLTGTGRISHGQVDLSLGPNADELKSKVEHIQIL 299
Db 246 GABAAADKGEYRHFMLKEIHEQPSVQVORTLEGLRQNVQMVYESFGPQAAELFAKVRNVQ 305
Qy 300 ACCTSNGMVSRYWFESLAGIPCDVEIASFEPRYKSAVRNLSMITLSQSGETADTLAAG 359
Db 306 ACCTSNGMVSRYWFESLAGIPCDVEIASFEPRYKSAVRNLSMITLSQSGETADTLA 365
Qy 360 LRLSKELGYLSLAICNVPGSSLVRESLALMTNAGTIGVASTKFTTQLTVLLMLVAK 419
Db 366 LRNAKELGFLSSVAICNVATSSLVRESDLTLLTQAGEIGVASTKFTTQLVALLLTGL 425
Qy 420 LSLR-KGLDASIEHDI VHGLQALPSRIEOMLSQDKRIEALAEFSDKXHALFLGRGDQY 478
Db 426 IGQVQKRLADGVEAEVDELRLRLPTRLGALAMNRTVEKVSSELPAEKHHTLFLGRGAQFP 485
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Qy	479	I A L E G A L K L K E I S Y I H A E Y A A G E L K H G P L A L I D A D M P V I V V A P N N E L L E K L K S N I E E V R	538
Db	486	V A L E G A L K L K E I S Y I H A E Y A P A G E L K H G P L A L V D S M P V V I V A P N N E L L E K L K S N I Q E V R	545
Qy	539	A R G G Q L Y V F A D Q A G F V S S D N M H I I E M P H V E E V I A F I F Y T V P L Q L L A Y H V A L I K G T D V D Q	598
Db	546	A R G G E L V F A D E G A G I E A G E T H V G M P H I G D V L S P I L Y T I P L Q L L S Y H V A V L K G T D V D Q	605
Qy	599	P R N L A K S V T V T E	609
Db	606	P R N L A K S V T V T E	616
RESULT 10			
US-09-328-352-5066			
; Sequence 5066, Application US/09328352			
; Patent No. 6562958			
; GENERAL INFORMATION:			
; APPLICANT: Gary L. Breton et al.			
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER			
; FILE REFERENCE: GTC99-03PA			
; CURRENT APPLICATION NUMBER: US/09/328,352			
; CURRENT FILING DATE: 1999-06-04			
; NUMBER OF SEQ ID NOS: 8252			
; SEQ ID NO 5066			
; LENGTH: 613			
; TYPE: PRT			
; ORGANISM: Acinetobacter baumannii			
US-09-328-352-5066			
Query Match 57.7%; Score 1780.5; DB 2; Length 613;			
Best Local Similarity 57.4%; Pred. No. 2.5e-166;			
Matches 353; Conservative 107; Mismatches 146; Indels 9; Gaps 5;			
Qy	1	M C G I V G A I A Q R D V A E I L L E G L R R L E Y R G Y D S A G L A V D A E G H M T R R L R L K G V Q M L A Q A A E	60
Db	2	M C G I V G V A E R C V T E I L E G L K E L Y R G Y D S A G V A L L N K Q - Q I L R E R R V G K V I N L E D A V A	60
Qy	61	E H P L H G T G T A H T R W A T H G E P S E V N A H P H V S E H I V V H N G I I E N H P L R E E L K A R G Y T V	120
Db	61	D Q O L T G T I G I A H T R W A T H G K T E N N A H P H M S G K V A V V H N G I I E N Y Q E L X D D L Q A L G Y V T	120
Qy	121	S E T D T E V I A H L V N W E L K O G G T L E A V L R A I P O L R G A Y G T V I M D S R H P D T L L A A R S G S P L A	180
Db	121	S Q T D T E V A H L A E A L K N T D S L L E A V S V P Q L K A Y A L G I H S D Y P D E L I T V R E G S P L V	180
Qy	181	I G L G M E N F T A S D Q L A L L P V T R R F I F L E E G D I A E I T R R S V N I P D K T G A E V K R Q D I E S N I Q	240
Db	181	I G V G I G E N F I S S D Q L A L L P V T N R F I Y L E E G D I A R L T R T S I E V F V K - G E R V E R P V K E L D A T	239
Qy	241	Y D A G D K G I Y R H Y M Q K E I Y E O P N A I K N T L T G R I S H G Q V D L S E L G P N A D E L L S K V E H I Q I L A	300
Db	240	V S S A S K G E Y K H Y M L K E I Y E O P E A I K O T I S Q A L D - G N N L R D D F L K D A E A D F S K L Q S V Q I T A	298
Qy	301	C G P S Y N S G M V S R Y W F E S L A G I P C D V E I A S E F R Y R K S A V R N S I M I T L S O S G E T A D T L A G L	360
Db	299	C G T S Y H S G M I A K Y W F Q L G V P C Q V E I A S E F R Y R S P V I V E N T L Y I C I S O S G E T A D T L A A L	358
Qy	361	R L S K E L C Y - - - - - L G S I A I C N V P G S S L V R E S D I A L M T N A G T E I G V A S T K A F T T Q L T V L I M	415
Db	359	R E T Q R A K A N N I D I Q T L I C N V A T S S W R E T D H H L T L A G P E I G V A S T K A F T T Q L A A L M L	418
Qy	416	L V A K L S R L K G L D A S I E - H D I V H G L Q A L P S R I E O M L S Q D K R I E A L A B D F S D K H A L F L G R G	474
Db	419	L I L K I G Q V K Q R I S N V M I E E L A R E L W H S P K V I L D T L Q D A E I L R S L S E L F V E K Q H C L F L G R G	478
Qy	475	D Q Y P I A L E G A L K L K E I S Y I H A E Y A A G E L K H G P L A L I D A D M P V I V V A P N N E L L E K L K S N I	534
Db	479	T H P I A L E G A L K L K E I S Y I H A E Y A A G E L K H G P L A L V D N E M P I V I L A P N D E M L D K L K S N M	538
Qy	535	E E V R A R G G Q L Y V F A D Q A G F V S S D N M H I I E M P H V E E V I A F I F Y T V P L Q L L A Y H V A L I K G T	594

Db	539	E E V Q A R G G E L F V F A D E N S G V E K D R Q H V Q I P A V N E W L A P I I Y S V P V Q L L S Y H V A V L R C T	598
Qy	595	D V D Q P R N L A K S V T V T E	609
Db	599	D V D Q P R N L A K S V T V T E	613
RESULT 11			
US-09-540-236-2182			
; Sequence 2182, Application US/09540236			
; Patent No. 6673910			
; GENERAL INFORMATION:			
; APPLICANT: Gary L. Breton et al.			
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARR			
; FILE REFERENCE: 2709.2005-001			
; CURRENT APPLICATION NUMBER: US/09/540,236			
; CURRENT FILING DATE: 2000-04-04			
; NUMBER OF SEQ ID NOS: 3840			
; SEQ ID NO 2182			
; LENGTH: 619			
; TYPE: PRT			
; ORGANISM: M. catarrhalis			
US-09-540-236-2182			
Query Match 48.4%; Score 1492.5; DB 2; Length 619;			
Best Local Similarity 50.3%; Pred. No. 6.8e-138;			
Matches 309; Conservative 112; Mismatches 186; Indels 7; Gaps 7;			
Qy	1	M C G I V G A I - A Q R D V A E I L L E G L R R L E Y R G Y S A G L A V D A E G H M T R R L R L K G V Q M L A Q A A	59
Db	8	M C G I V G A I R T H N V D F L T D G L K L E Y R G Y D S S G I A - V Q T E S G I R R V A R V G R V A L M E E A A	66
Qy	60	B E H P L H G T G T A H T R W A T H G E P S E V N A H P H V S E H I V - V H N G I I E N H P L R E E L K A R G Y T	118
Db	67	K Q K Q I H G L T G I C H T R W A T H G V T K P N A H P H I S A G L I S V V H N G I I E N F E T E R L Q H L D Y E	126
Qy	119	F V S E T D T E V I A H L V N W E - L K O G G T L R E A V L R A I P O L R G A Y G T V I M D S R H P D T L L A A R S G S	177
Db	127	F E S Q T D T E V I A H S V H Q E Y T T N G G D L Y H A V Q T A C S R F H G A Y A I A V A N D A P N Q M V T A R M G C	186
Qy	178	P L V I G L G M E N F I A S D Q L A L L P V T R R F I F L E E G D I A E I T R R S V - N I P D K T G A E V K R Q D I E	236
Db	187	P L L V A F A G D N E V F A S D V S A V T A F T R R V T Y L E D G D I A L L Q A D G I O K L L D K D G N Q V N R S I K T	246
Qy	237	S N L Q V D A G D K G I Y R H Y M Q K E I Y E O P N A I K N T L T G R I S H G Q V D L S E L G P N A D E L L S K V E H I	296
Db	247	S E M S I A S L E L G P Y S H F M Q K E I N E O P R A V S D T A E I F L E G G F V - A D N F G E A P E I F A K I Q S I	305
Qy	297	Q I L A C G T S Y N S G M V S R Y W F E S L A G I P C D V E I A S E F R Y R K S A V R R N S I M I T L S O S G E T A D T	356
Db	306	K I L A C G T S Y A A L T G K Y L E S I A K I R C D V E I A S E Y R Y R D V I S D P D E L V I T T S O S G E T L D T	365
Qy	357	L A G L R L S K E L G Y L G S L A I C N V P G S S L V R E S D I A L M T N A G T E I G V A S T K A F T T Q L T V L I M L	416
Db	366	M E A L K Y A N A Q H R Y S L S I C N V M E S A L P R T S T L A I F T R A G A E I G V A S T K A F T T Q L V V L F C L	425
Qy	417	V A K L S R L K G - I D A S I E H D I V H G L Q A L P S R I E O M L S Q D K R I E A L A B D F S D K H A L F L G R G D	475
Db	426	A V T L G I L R H G V D E S Q A Q Y A E D L R L L P G S I Q H A L N L E P Q L A S W A Q S F A N K F S A L F L G R G I	485
Qy	476	C Y P T A L E G A L K L K E I S Y I H A E Y A A G E L K H G P L A L I D A D M P V I V V A P N N E L L E K L K S N I E	535
Db	486	H Y P T A L E G A L K L K E I Y I H A E S Y P A G E L K H G P L A L V D N E M P V V I S P N D G L L D K R Y A N N Q	545
Qy	536	E V R A R G G Q L Y V F A D Q A G F V S S D N M H I I E M P H V E E V I A F I F Y T V P L Q L L A Y H V A L I K G T D	595
Db	546	E V S A R G G E L F V L S D L D S D Y T A S E G V H I R T P R H I G T L S P I V H T I P V Q L L A Y H V A L V K G T D	605
Qy	596	V D Q P R N L A K S V T V T E	609
Db	606	V D K P R N L A K S V T V T E	619

RESULT 12
US-09-902-540-16012
; Sequence 16012, Application US/0902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16012
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16012

Query Match 44.2%; Score 1362.5; DB 2; Length 572;
Best Local Similarity 50.0%; Pred. No. 4e-125;
Matches 279; Conservative 105; Mismatches 161; Indels 13; Gaps 7;
QY 59 AEHPLHGGTGIATRWATHGEPSEVNAHPHSEHIVVHNGIENHEPRLBELKARGYT 118
DB 21 ADQPP--GNIGIGHTRWATHGRPSDENAHPTTYKDVAVVHNGIENHLSLKEQURSGHV 78
QY 119 FVSETDTEVIAHLVNNELKGGTLREAVLRAIPQLRGAYGTVMDSRHPDPTLLAARSGP 178
DB 79 FSSETSEVFAHIISELENGLELPDRAVRAIAQVGTVALAVLTASDFSRVCTKDASP 138
QY 179 LVIGLGMGFNTASDQALLPVTRRFIFLEEGDIAETRISVNI FDKTGAEVKRODIESN 238
DB 139 MVGLGQGNFLASDVPALLEHTRDFVYMEEGDLAVITAAVDIFNRQGVNRPTRRID 198
QY 239 LQYDAGDKGIYHYMQKEIYEQNAINKNTLTGR--ISHGVDSLSELGPNADLLSKVEHI 296
DB 199 WTPMAEKGGKHFMHKEIWEQPRVADTLRGRMLLSEGDVHPEGNLSAEKVRS-LTKI 257
QY 297 QILACGTSYNSGMVSRVWFESLAGIPCDVEIASEFRYKSAVRNSIMITLSQSGETADT 356
DB 258 TILACGTSWHSGVAGKHMIESLARLPVEVELASEFRYRDPIDVGTHLAIAISQSGETADT 317
QY 357 LAGLRSLKELGYLGSLAICNPVGSLSVRSDALMTNAGTEIGVASTKFTTOLTLLML 416
DB 318 LAAFKEAKARG-ATANAI CNVIGSAMTREADFSVLINAGPEIGVASTKFTTOLVALFLL 376
QY 417 VAKLSRLKG---LDASIEHDIHVLGQALPSRIEQLSODKRIEALAEFSDKHHLFLGR 473
DB 377 AVKLGSRMRGTLSPAAQEH--LTQLTKVPKMIEDVLKCEPAVTRVSRVYMSQDFLFLGR 434
QY 474 GDQYPTALEGALKKEISYTHABAYAGELKHGFLALIDADMPVIVVAPN--NELLEK 531
DB 435 GMPHPVALLGALKKEISYTHABAYAGELKHGFLALIDADMPVIVVAPN--NELLEK 494
QY 532 SNTVEEVRAGGQLYVFADQAGVPSVNDNMHIEMPHVEEVIAPFTVPLQLLAYHVALI 591
DB 495 GNIEEVRAGGKVIADIDEDDEHVALQDVITRIPACALLAPVAVTIFLQLLAYHVAL 554
QY 592 KGTVDQPNRLAKSVTVE 609
DB 555 RGNVDQPNRLAKSVTVE 572

RESULT 13
US-08-599-171A-30
; Sequence 30, Application US/08599171A
; Patent No. 5814473

; GENERAL INFORMATION:
; APPLICANT: WARREN, Patrick V.
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,171A
; FILING DATE: Concurrently
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: HERRON, CHARLES J.
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 331400-38
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 592 AMINO ACIDS
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
US-08-599-171A-30

Query Match 44.0%; Score 1357.5; DB 1; Length 592;
Best Local Similarity 46.5%; Pred. No. 1.3e-124;
Matches 286; Conservative 113; Mismatches 187; Indels 29; Gaps 9;
QY 1 MCGIIVCAIQRDVA-EILLEGRLRYRGVDSAGLAVDAEGHMTLRRLRGKVOMLAQAA 59
DB 1 MCGIIVGVG-RDLALPVIIGALERLEYRGYDSAGVALIE-DGKLIVKKGKIRLKV 58
QY 60 EEHPLHGGTGIATRWATHGEPSEVNAHPHSE--HIVVHNGIENHEPRLBELKARG 117
DB 59 WKNDYKAKTGIGTRWATHGKPTDENAHPTDEKGEFAVHNGIENYLELKEELKEGV 118
QY 118 TVFSETDTEVIAHLVNNELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDPTLLAARSG 177
DB 119 KFRSETDTEVIAHLIAKNYR--GDLLEAVLKTVKLKGAFATVTHPEPNRLIGVKQS 176
QY 178 PLVIGLGMGFNTASDQALLPVTRRFIFLEEGDIAETRISVNI FDKTGAEVKRODIES 237
DB 177 PLVIGLGMGFNTASDQALLPVTRRFIFLEEGDIAETRISVNI FDKTGAEVKRODIES 236
QY 238 NLQYDAGDKGIYHYMQKEIYEQNAINKNTLTGRISHGVDSLSELGPNADL---LSKVE 294
DB 237 PNDLSAEKGGKHPMLKEIYEQPKAINDTLKGFLS-----TEDAIFPKLKDPR 295
QY 295 HIQILACGTSYNSGMVSRVWFESLAGIPCDVEIASEFRYKSAVRNSIMITLSQSGETA 354
DB 286 RVLIIACGTSYHAGFVGKYWIERFAGVPTVEIYASEFRYADVPVSDKDIVIGISQSGETA 345
QY 355 DTLAGLRSLKELGYLGSLAICNPVGSLSVRSDALMTNAGTEIGVASTKFTTOLTLL 414
DB 346 DTKFALQSAKEGAF-TVGLVNVVGSADIDRESLSLHTHAGPEIGVAAKTFTFAQTALY 404
QY 415 MLVAKLSRLKGLDASIEHDIHVLGQALPSRIEQLSODKRIEALAEFSDKHHLFLGR 474

Db 405 ALSVR-----ESEERENLRLEKVPESLVEQTLNTEAEVEKVAEKYMKKQWLYLGRY 457
QY 475 DOYPALLEGALKLKEISYIHAEEYAAGELKHGPIALIDAMPVIVVAPNNELLEKLKSN 534
Db 458 LNYPIALEGALKLKEISYIHAEGYPAGEMKHGPITALIDENNPVVVVIAPKDRVVEKILSNV 517
QY 535 BEVRARGQLVVFADQDAGFVSSDNMHIEMPHVEEVIAPIFYTVPLQLLAYHVALIKGT 594
Db 518 EEVLARKGRVISVGFKGDETLKSKSESVMIEPKAEBEIPITPFLTVPQLFAYFIASKLGL 577
QY 595 DVDQPRNLAKSVTVE 609
Db 578 DVDQPRNLAKTVTVE 592

RESULT 14
US-08-646-590B-30
; Sequence 30, Application US/08646590B
; Patent No. 5962283
; GENERAL INFORMATION:
; APPLICANT: Warren, Patrick V.
; APPLICANT: Swanson, Ronald V.
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: US
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/646,590B
; FILING DATE: 08-May-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,171
; FILING DATE: 09-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/01094
; FILING DATE: 21-January-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Liea A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 592 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-08-646-590B-30

Query Match 44.0%; Score 1357.5; DB 1; Length 592;
Best Local Similarity 46.5%; Pred. No. 1.3e-124;
Matches 286; Conservative 113; Mismatches 187; Indels 29; Gaps 9;

QY 1 MCGIVGAIAORDVA-BILLEGLRLRYGVDSAGLAVVDAGHMTLRRLRGVQVQLAQA 59
Db 1 MCGIVGVG-RDALPIVIGALERLEYRGYDSAGVALIE-DKGLIVEKKGKIRELVKAL 58
QY 60 EEHPLHGGTGIATRWATHGEPSEVNAHPHVS--HIVVHNGIIEHNEPLREELKARGY 117

Db 59 WCKDYKAKTGIGHTRWATHGKETDENAHPTDEKGEFAVVHNGIIEYIELKEELKQGV 118
QY 118 TFSVSETDEVIHVLNWLKQGTTLREAVLRAIPQLRGAYGTVIMDSRHPDITLLAARSGS 177
Db 119 KFRSETDTEVIAHLIAKNYR--GDLEAVLTKVKLKGAFAPAVITVHPEPNLIGVKQGS 176
QY 178 PLVIGLHGENFIASDQALALLPVTRFRFPLEBGDIAETITRRSVNIPDKTGAEVKQODIES 237
Db 177 PLVIGLGEENFLASDIPAILFPYTKKIIIVLDDGEIADLTPTDVTNINFEFEPVSEVMIT 236
QY 238 NLQYDAGDKGIYRHYMOKEIYBOPNAIKNTLTGRISHGQVDLSLSELGPNADL--LSKVE 294
Db 237 PWDLSAEGGFKHFMLEIYEQPKAINDTLKGLS-----TEDAIPFKLKDFR 285
QY 295 HIQILACGTSYNSGMVSRYWFSFESLAGIPCDVEIASEPRYKSAVRNLSMITLSQGETA 354
Db 286 RVLIIACGTSYHAGFVGKWIETPAGVPTVIYASEPRYADVPSDKDVIIGISQGETA 345
QY 355 DTLAGLRLSKELGYLSLAI CNVPOSSLVRESDLALMTNAGTEIGVASTKAPTOLTVL 414
Db 346 DTKFALQSAKEKGAF-TVGLVNVVGSADRESDFSLSHTHAGPEIGVAATKTFTAQFTALY 404
QY 415 MLVAKLSRLKGLDASIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEDFSDKHHALFLGRG 474
Db 405 ALSVR-----ESEERENLRLEKVPESLVEQTLNTEAEVEKVAEKYMKKQWLYLGRY 457
QY 475 DOYPALLEGALKLKEISYIHAEEYAAGELKHGPIALIDAMPVIVVAPNNELLEKLKSN 534
Db 458 LNYPIALEGALKLKEISYIHAEGYPAGEMKHGPITALIDENNPVVVVIAPKDRVVEKILSNV 517
QY 535 BEVRARGQLVVFADQDAGFVSSDNMHIEMPHVEEVIAPIFYTVPLQLLAYHVALIKGT 594
Db 518 EEVLARKGRVISVGFKGDETLKSKSESVMIEPKAEBEIPITPFLTVPQLFAYFIASKLGL 577
QY 595 DVDQPRNLAKSVTVE 609
Db 578 DVDQPRNLAKTVTVE 592

RESULT 15
US-09-069-226-30
; Sequence 30, Application US/09069226
; Patent No. 6013509
; GENERAL INFORMATION:
; APPLICANT: WARREN, Patrick V.
; TITLE OF INVENTION: TRANSAMINASES AND AMINOTRANSFERASES
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/069,226
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/599,171
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: HERRON, CHARLES J.
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 331400-38
; TELECOMMUNICATION INFORMATION:

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 7, 2006, 09:26:41 ; Search time 93 Seconds
(without alignments)
3033.310 Million cell updates/sec

Title: US-10-612-779-2

Perfect score: 3086

Sequence: 1 MCGIVGAIQRDVAEILLEG.....LIKGTDVDPRLAKSVTVE 609

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:*

- 1: /EMC_Celerra_SID83/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SID83/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SID83/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SID83/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
- 5: /EMC_Celerra_SID83/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SID83/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3086	100.0	609	3	US-09-815-242-10399 Sequence 10399, A
2	3086	100.0	609	4	US-10-024-460-16 Sequence 16, Appl
3	3086	100.0	609	4	US-10-369-493-23611 Sequence 23611, A
4	3086	100.0	609	4	US-10-282-122A-56753 Sequence 56753, A
5	3086	100.0	609	4	US-10-612-779-2 Sequence 2, Appl
6	3086	100.0	609	5	US-10-823-397-23 Sequence 23, Appl
7	3080	99.8	609	4	US-10-024-460-28 Sequence 28, Appl
8	3080	99.8	609	4	US-10-024-460-31 Sequence 31, Appl
9	3080	99.8	609	4	US-10-612-779-10 Sequence 10, Appl
10	3080	99.8	609	4	US-10-612-779-12 Sequence 12, Appl
11	3079	99.8	609	4	US-10-024-460-25 Sequence 25, Appl
12	3079	99.8	609	4	US-10-612-779-8 Sequence 8, Appl
13	3071	99.5	609	4	US-10-024-460-19 Sequence 19, Appl
14	3071	99.5	609	4	US-10-612-779-4 Sequence 4, Appl
15	3068	99.4	609	4	US-10-024-460-22 Sequence 22, Appl
16	3068	99.4	609	4	US-10-612-779-6 Sequence 6, Appl
17	3068	99.4	609	5	US-10-823-397-25 Sequence 25, Appl
18	3061	99.2	609	4	US-10-612-779-14 Sequence 14, Appl
19	3053	98.9	609	3	US-09-815-242-14065 Sequence 14065, A
20	3053	98.9	609	4	US-10-282-122A-76152 Sequence 76152, A
21	2950	95.6	609	4	US-10-282-122A-56279 Sequence 56279, A
22	2876	93.2	609	3	US-09-815-242-11758 Sequence 11758, A
23	2871	93.0	609	4	US-10-282-122A-59335 Sequence 59335, A
24	2718.5	88.1	608	4	US-10-282-122A-72965 Sequence 72965, A
25	2682	86.9	609	4	US-10-282-122A-78533 Sequence 78533, A
26	2661	86.2	609	4	US-10-369-493-21242 Sequence 21242, A
27	2619	84.9	609	4	US-10-369-493-438 Sequence 438, App

ALIGNMENTS

RESULT 1

US-09-815-242-10399
; Sequence 10399, Application US/09815242
; Patent No. US20020061569A1

GENERAL INFORMATION:

- ; APPLICANT: Hasebeck, Robert
- ; APPLICANT: Ohlsen, Kari L.
- ; APPLICANT: Zyskind, Judith W.
- ; APPLICANT: Wall, Daniel
- ; APPLICANT: Trawick, John D.
- ; APPLICANT: Carr, Grant J.
- ; APPLICANT: Yamamoto, Robert T.
- ; APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITPA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10399

LENGTH: 609

TYPE: PRT

ORGANISM: Escherichia coli

US-09-815-242-10399

Query Match 100.0%; Score 3086; DB 3; Length 609;

Best Local Similarity 100.0%; Pred. No. 4.7e-249;

Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQRDVAEILLEGRLRYGYDSAGLVAVDAGHMTLRRLKGVQMLAAAE 60

Db 1 MCGIVGAIQRDVAEILLEGRLRYGYDSAGLVAVDAGHMTLRRLKGVQMLAAAE 60

Qy 61 EPHLHGCTGTATRWATHGSEPNAPHYSEHVIVVHNGIENHEPLREELKARGYTFV 120

Db 61 EHPLHGGTGAIAHTRWATHGEPSEVNAHPHVSEHIVVHNGIIEHNHEPLREELKARGYTFV 120
QY 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPOLRGAYGTVMDSRHPDPTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPOLRGAYGTVMDSRHPDPTLLAARSGSPLV 180
QY 181 IGLGNGENFIASDQALLPVTRRFIFLEEGDIAEITRRSVNIIPDKTGAEVKRODIESNLQ 240
Db 181 IGLGNGENFIASDQALLPVTRRFIFLEEGDIAEITRRSVNIIPDKTGAEVKRODIESNLQ 240
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Db 241 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSLSELGNADDELLSKVEHIQILA 300
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Db 301 CGTSYNSGMVSRWYFESLAGIPCDVEIASFEFRYKSAVRNSLMITLSQSGETADTLAGL 360
QY 361 RLSKELGYLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAPTQTOLTVLMLVAKL 420
Db 361 RLSKELGYLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAPTQTOLTVLMLVAKL 420
QY 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEFDSKHALFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEFDSKHALFLGRGDQYPIA 480
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Db 481 LEGALKLKEISYTHAEAYAAAGELKHGPIALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
QY 541 GGOLYVPADQAGFVSSDNMHIIEMPHVEEVIAPIFTYVPLQLLAYHVALIKGTDVDQPR 600
Db 541 GGOLYVPADQAGFVSSDNMHIIEMPHVEEVIAPIFTYVPLQLLAYHVALIKGTDVDQPR 600
QY 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 2

US-10-024-460-16
; Sequence 16, Application US/10024460
; Publication No. US20030044939A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/10/024,460
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-024-460-16

Query Match 100.0%; Score 3086; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.7e-249;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCGIVGAIAQRDVAEIILLEGRLREYRGYDSAGLAVDAEGHMTLRRLRGKQVQLAQAAE 60
Db 1 MCGIVGAIAQRDVAEIILLEGRLREYRGYDSAGLAVDAEGHMTLRRLRGKQVQLAQAAE 60
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Db 61 EHPLHGGTGAIAHTRWATHGEPSEVNAHPHVSEHIVVHNGIIEHNHEPLREELKARGYTFV 120
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Db 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPOLRGAYGTVMDSRHPDPTLLAARSGSPLV 180
QY 181 IGLGNGENFIASDQALLPVTRRFIFLEEGDIAEITRRSVNIIPDKTGAEVKRODIESNLQ 240
Db 181 IGLGNGENFIASDQALLPVTRRFIFLEEGDIAEITRRSVNIIPDKTGAEVKRODIESNLQ 240
QY 241 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSLSELGNADDELLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSLSELGNADDELLSKVEHIQILA 300
QY 301 CGTSYNSGMVSRWYFESLAGIPCDVEIASFEFRYKSAVRNSLMITLSQSGETADTLAGL 360
Db 301 CGTSYNSGMVSRWYFESLAGIPCDVEIASFEFRYKSAVRNSLMITLSQSGETADTLAGL 360
QY 361 RLSKELGYLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAPTQTOLTVLMLVAKL 420
Db 361 RLSKELGYLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAPTQTOLTVLMLVAKL 420
QY 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEFDSKHALFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEFDSKHALFLGRGDQYPIA 480
QY 481 LEGALKLKEISYTHAEAYAAAGELKHGPIALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
Db 481 LEGALKLKEISYTHAEAYAAAGELKHGPIALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
QY 541 GGOLYVPADQAGFVSSDNMHIIEMPHVEEVIAPIFTYVPLQLLAYHVALIKGTDVDQPR 600
Db 541 GGOLYVPADQAGFVSSDNMHIIEMPHVEEVIAPIFTYVPLQLLAYHVALIKGTDVDQPR 600
QY 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 3

US-10-369-493-23611
; Sequence 23611, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 23611
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-369-493-23611

Query Match 100.0%; Score 3086; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.7e-249;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCGIVGAIAQRDVAEIILLEGRLREYRGYDSAGLAVDAEGHMTLRRLRGKQVQLAQAAE 60
Db 1 MCGIVGAIAQRDVAEIILLEGRLREYRGYDSAGLAVDAEGHMTLRRLRGKQVQLAQAAE 60
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Db 61 EHPHGGTGIAHTRWATHGEPSEVNAHPHVSEHIVVVHNGIIENHPELREELKARGYTFV 120
QY 121 SETDTEVIAHLVNMELKQGGLREAVLRAIPQURGAYGTVMDSRHPDITLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNMELKQGGLREAVLRAIPQURGAYGTVMDSRHPDITLLAARSGSPLV 180
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Db 181 IGLGMGENFIASDQALLPVTRRFIFLEEGDIAEITRRSVNIIPDKTGAEVKRDIESNLQ 240
QY 241 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSSELGNADDELLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSSELGNADDELLSKVEHIQILA 300
QY 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNSLMTLSQSGETADTLAGL 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNSLMTLSQSGETADTLAGL 360
QY 361 RLSKELGYLGSGLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQLTVLLMLVAKL 420
Db 361 RLSKELGYLGSGLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQLTVLLMLVAKL 420
QY 421 SRLKGLDASTIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEFSDKHHALFLGRGDQYPIA 480
Db 421 SRLKGLDASTIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEFSDKHHALFLGRGDQYPIA 480
QY 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
Db 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
QY 541 GGOLYVFADQDAGFVSSDNNHIIEMPHVEEVIAPIFTVPLQLLAVHVALIKGTDVDDQPR 600
Db 541 GGOLYVFADQDAGFVSSDNNHIIEMPHVEEVIAPIFTVPLQLLAVHVALIKGTDVDDQPR 600
QY 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 4
US-10-282-122A-56753
; Sequence 56753, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zvakind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56753
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-10-282-122A-56753

Query Match 100.0%; Score 3086; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 4,7e-249;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MCGIVGAIQAORDVAEILLEGRLREYRGYDSAGLAVVDAEGHMTLRRLRGKVQMLAQAAE 60
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Db 61 EHPHGGTGIAHTRWATHGEPSEVNAHPHVSEHIVVVHNGIIENHPELREELKARGYTFV 120
QY 121 SETDTEVIAHLVNMELKQGGLREAVLRAIPQURGAYGTVMDSRHPDITLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNMELKQGGLREAVLRAIPQURGAYGTVMDSRHPDITLLAARSGSPLV 180
QY 181 IGLGMGENFIASDQALLPVTRRFIFLEEGDIAEITRRSVNIIPDKTGAEVKRDIESNLQ 240
Db 181 IGLGMGENFIASDQALLPVTRRFIFLEEGDIAEITRRSVNIIPDKTGAEVKRDIESNLQ 240
QY 241 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSSELGNADDELLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSSELGNADDELLSKVEHIQILA 300
QY 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNSLMTLSQSGETADTLAGL 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNSLMTLSQSGETADTLAGL 360
QY 361 RLSKELGYLGSGLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQLTVLLMLVAKL 420
Db 361 RLSKELGYLGSGLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQLTVLLMLVAKL 420
QY 421 SRLKGLDASTIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEFSDKHHALFLGRGDQYPIA 480
Db 421 SRLKGLDASTIEHDIHVHGLQALPSRIEQMLSDQKRIEALAEFSDKHHALFLGRGDQYPIA 480
QY 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
Db 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEVRAR 540
QY 541 GGOLYVFADQDAGFVSSDNNHIIEMPHVEEVIAPIFTVPLQLLAVHVALIKGTDVDDQPR 600
Db 541 GGOLYVFADQDAGFVSSDNNHIIEMPHVEEVIAPIFTVPLQLLAVHVALIKGTDVDDQPR 600
QY 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 5
US-10-612-779-2
; Sequence 2, Application US/10612779
; Publication No. US20040091976A1
; GENERAL INFORMATION:
; APPLICANT: Deng, Ming-De
; APPLICANT: Angerer, J. David
; APPLICANT: Cyron, Don

APPLICANT: Grund, Alan
APPLICANT: Jerrell Jr., Thomas
APPLICANT: Leanna, Candice
APPLICANT: Mathre, Owen
APPLICANT: Robson, Reinhardt
APPLICANT: Running, Jeff
APPLICANT: Severson, Dave
APPLICANT: Song, Linsheng
APPLICANT: Wasink, Sarah
TITLE OF INVENTION: Process and Materials for Production of Glucosamine and N-Acetylg
TITLE OF INVENTION: Glucosamine
FILE REFERENCE: 3161-18-2
CURRENT APPLICATION NUMBER: US/10/612,779
CURRENT FILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: 60/393,348
PRIOR FILING DATE: 2002-07-01
NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 609
TYPE: PRT
ORGANISM: Escherichia coli
US-10-612-779-2

Query Match 100.0%; Score 3086; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.7e-249;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MCGIVGAIARDVNAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRRLRGKVQMLAAQAE 60
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Qy 61 EPHLGGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHPELREELKARGYTFV 120
Db 61 EPHLGGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHPELREELKARGYTFV 120
Qy 121 SETDTEVIAHLVNMELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDTLLAARSGSLV 180
Db 121 SETDTEVIAHLVNMELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDTLLAARSGSLV 180
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Db 181 IGLGMENFTASDQALLPVTRRFIFLEEGDIAEITRRSVNIPDKTGAEVKQDIESNLQ 240
Qy 241 YDAGDKGIYHYMOKEIEYQPNAIKNTLTGRISHGOVDLSLGNADLLSKVEHIQILA 300
Db 241 YDAGDKGIYHYMOKEIEYQPNAIKNTLTGRISHGOVDLSLGNADLLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASBFYRKSAVRNLSMITLSQSGETADTLA 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASBFYRKSAVRNLSMITLSQSGETADTLA 360
Qy 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLTVLLMLVAKL 420
Db 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLTVLLMLVAKL 420
Qy 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSQDKRIEALAEFSDKHALLFLGRGDQYPTA 480
Db 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSQDKRIEALAEFSDKHALLFLGRGDQYPTA 480
Qy 481 LEGALKLKEISYTHAEYAAAGELKHGPLALIDADMPVIVVAPNNELLEKLSNIEVRAR 540
Db 481 LEGALKLKEISYTHAEYAAAGELKHGPLALIDADMPVIVVAPNNELLEKLSNIEVRAR 540
Qy 541 GGQLYVFAQQDAGFVSSDNHIIEMPHVEEVIAPIFTYVPLQLLAYHVALIKGTDVDDPR 600
Db 541 GGQLYVFAQQDAGFVSSDNHIIEMPHVEEVIAPIFTYVPLQLLAYHVALIKGTDVDDPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609
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RESULT 7

RESULT 6
US-10-823-397-23
Sequence 23, Application US/10823397
Publication No. US20050042735A1
GENERAL INFORMATION:
APPLICANT: McMullin, Thomas
APPLICANT: Ding, Ming-De
APPLICANT: Grund, Alan
TITLE OF INVENTION: Metabolic Engineering for Enhanced Production of Chitin and
TITLE OF INVENTION: Chitosan in Microorganisms
FILE REFERENCE: 3161-18-3
CURRENT APPLICATION NUMBER: US/10/823,397
CURRENT FILING DATE: 2004-04-12
PRIOR APPLICATION NUMBER: 60/462,087
PRIOR FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 609
TYPE: PRT
ORGANISM: Escherichia coli
US-10-823-397-23

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Qy 1 MCGIVGAIARDVNAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRRLRGKVQMLAAQAE 60
Db 1 MCGIVGAIARDVNAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRRLRGKVQMLAAQAE 60
Qy 61 EPHLGGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHPELREELKARGYTFV 120
Db 61 EPHLGGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHPELREELKARGYTFV 120
Qy 121 SETDTEVIAHLVNMELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDTLLAARSGSLV 180
Db 121 SETDTEVIAHLVNMELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDTLLAARSGSLV 180
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Db 181 IGLGMENFTASDQALLPVTRRFIFLEEGDIAEITRRSVNIPDKTGAEVKQDIESNLQ 240
Qy 241 YDAGDKGIYHYMOKEIEYQPNAIKNTLTGRISHGOVDLSLGNADLLSKVEHIQILA 300
Db 241 YDAGDKGIYHYMOKEIEYQPNAIKNTLTGRISHGOVDLSLGNADLLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASBFYRKSAVRNLSMITLSQSGETADTLA 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASBFYRKSAVRNLSMITLSQSGETADTLA 360
Qy 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLTVLLMLVAKL 420
Db 361 RLSKELGYLGLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKFTTQTLTVLLMLVAKL 420
Qy 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSQDKRIEALAEFSDKHALLFLGRGDQYPTA 480
Db 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSQDKRIEALAEFSDKHALLFLGRGDQYPTA 480
Qy 481 LEGALKLKEISYTHAEYAAAGELKHGPLALIDADMPVIVVAPNNELLEKLSNIEVRAR 540
Db 481 LEGALKLKEISYTHAEYAAAGELKHGPLALIDADMPVIVVAPNNELLEKLSNIEVRAR 540
Qy 541 GGQLYVFAQQDAGFVSSDNHIIEMPHVEEVIAPIFTYVPLQLLAYHVALIKGTDVDDPR 600
Db 541 GGQLYVFAQQDAGFVSSDNHIIEMPHVEEVIAPIFTYVPLQLLAYHVALIKGTDVDDPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609
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US-10-024-460-28
; Sequence 28, Application US/10024460
; Publication No. US20030044939A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/10/024,460
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 609
; TYPE: PR1
; ORGANISM: Escherichia coli
US-10-024-460-28

Query Match 99.8%; Score 3080; DB 4; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.5e-248;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIARDVAEILLEGRLREYRGYSAGLAVVDAEGHMTLRLRLGKVQMLAAAE 60
Db 1 MCGIVGAIARDVAEILLEGRLREYRGYSAGLAVVDAEGHMTLRLRLGKVQMLAAAE 60

Qy 61 EPHLGGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHNEPLREELKARGYTFV 120
Db 61 EPHLGGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHNEPLREELKARGYTFV 120

Qy 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPLV 180

Qy 181 IGLGMENFTASDQALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRODIESNLQ 240
Db 181 IGLGMENFTASDQALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRODIESNLQ 240

Qy 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADLLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADLLSKVEHIQILA 300

Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNLSMITLSQSGETADTLA 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNLSMITLSQSGETADTLA 360

Qy 361 RLSKELGYLGS LAICNVPGSSLVRESLALMTNAGTEIGVASTKAFPTTQTLTVLLMLVAKL 420
Db 361 RLSKELGYLGS LAICNVPGSSLVRESLALMTNAGTEIGVASTKAFPTTQTLTVLLMLVAKL 420

Qy 421 SRLKGLDASIEHDI VHGLQALPSRIEOMLSODKRIEALAEFSDKXHALFLRGDQYPIA 480
Db 421 SRLKGLDASIEHDI VHGLQALPSRIEOMLSODKRIEALAEFSDKXHALFLRGDQYPIA 480

Qy 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLSNIEEVRAR 540
Db 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLSNIEEVRAR 540

Qy 541 GGQLYVPADQAGFVSDNNHIIEMPHVEEVIAPIFVTVPLQLLAYHVALIKGTDVQDPR 600
Db 541 GGQLYVPADQAGFVSDNNHIIEMPHVEEVIAPIFVTVPLQLLAYHVALIKGTDVQDPR 600

Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

US-10-024-460-31
; Sequence 31, Application US/10024460
; Publication No. US20030044939A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/10/024,460
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 609
; TYPE: PR1
; ORGANISM: Escherichia coli
US-10-024-460-31

Query Match 99.8%; Score 3080; DB 4; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.5e-248;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIARDVAEILLEGRLREYRGYSAGLAVVDAEGHMTLRLRLGKVQMLAAAE 60
Db 1 MCGIVGAIARDVAEILLEGRLREYRGYSAGLAVVDAEGHMTLRLRLGKVQMLAAAE 60

Qy 61 EPHLGGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHNEPLREELKARGYTFV 120
Db 61 EPHLGGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIIEHNEPLREELKARGYTFV 120

Qy 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPLV 180

Qy 181 IGLGMENFTASDQALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRODIESNLQ 240
Db 181 IGLGMENFTASDQALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRODIESNLQ 240

Qy 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADLLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADLLSKVEHIQILA 300

Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNLSMITLSQSGETADTLA 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNLSMITLSQSGETADTLA 360

Qy 361 RLSKELGYLGS LAICNVPGSSLVRESLALMTNAGTEIGVASTKAFPTTQTLTVLLMLVAKL 420
Db 361 RLSKELGYLGS LAICNVPGSSLVRESLALMTNAGTEIGVASTKAFPTTQTLTVLLMLVAKL 420

Qy 421 SRLKGLDASIEHDI VHGLQALPSRIEOMLSODKRIEALAEFSDKXHALFLRGDQYPIA 480
Db 421 SRLKGLDASIEHDI VHGLQALPSRIEOMLSODKRIEALAEFSDKXHALFLRGDQYPIA 480

Qy 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLSNIEEVRAR 540
Db 481 LEGALKLKEISYTHAEAYAGELKHGPLALIDAMPVIVVAPNNELLEKLSNIEEVRAR 540

Qy 541 GGQLYVPADQAGFVSDNNHIIEMPHVEEVIAPIFVTVPLQLLAYHVALIKGTDVQDPR 600
Db 541 GGQLYVPADQAGFVSDNNHIIEMPHVEEVIAPIFVTVPLQLLAYHVALIKGTDVQDPR 600

Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

US-10-612-779-10
; Sequence 10, Application US/10612779
; Publication NO. US20040091976A1
; GENERAL INFORMATION:
; APPLICANT: Deng, Ming-De
; APPLICANT: Angerer, J. David
; APPLICANT: Cyron, Don
; APPLICANT: Grund, Alan
; APPLICANT: Jerrell Jr., Thomas
; APPLICANT: Leanna, Candice
; APPLICANT: Mathre, Owen
; APPLICANT: Rosson, Reinhardt
; APPLICANT: Running, Jeff
; APPLICANT: Severson, Dave
; APPLICANT: Song, Linsheng
; APPLICANT: Wassink, Sarah
; TITLE OF INVENTION: Process and Materials for Production of Glucosamine and N-Acetyls
; FILE REFERENCE: 3161-18-2
; CURRENT APPLICATION NUMBER: US/10/612,779
; CURRENT FILING DATE: 2003-07-01
; PRIOR FILING DATE: 2003-07-01
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-612-779-10

Query Match 99.8%; Score 3080; DB 4; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.5e-248;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQAORDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRRLRGKVMQLAAAE 60
Db 1 MCGIVGAIQAORDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRRLRGKVMQLAAAE 60

Qy 61 EPHLGCGTGAIAHTRWATHGPESEVNAHPHVSEHIVVHNGIIEHHEPLREELKARGYTFV 120
Db 61 EPHLGCGTGAIAHTRWATHGPESEVNAHPHVSEHIVVHNGIIEHHEPLREELKARGYTFV 120

Qy 121 SETDTEVIAHLVNMWELKQGGTLREAVLRAIPQURGAYGTVMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNMWELKQGGTLREAVLRAIPQURGAYGTVMDSRHPDTLLAARSGSPLV 180

Qy 181 IGLGMENFIASDQALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKQDIESNLQ 240
Db 181 IGLGMENFIASDQALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKQDIESNLQ 240

Qy 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADLLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADLLSKVEHIQILA 300

Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFEFRYKSAVRNSLMITLSQSGETADTLAGL 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFEFRYKSAVRNSLMITLSQSGETADTLAGL 360

Qy 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQTLTVLLMLVAKL 420
Db 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQTLTVLLMLVAKL 420

Qy 421 SRLKGLDASTEHIDVHGLQALPSRIEOMLSQDKRIEALAEFSDKHAFILGRGQDYPYA 480
Db 421 SRLKGLDASTEHIDVHGLQALPSRIEOMLSQDKRIEALAEFSDKHAFILGRGQDYPYA 480

Qy 481 LEGALKLKEISYTHAAYAGELKHGFLALIDADMPVIVVAPNNLEKLSKNIIEVRAR 540
Db 481 LEGALKLKEISYTHAAYAGELKHGFLALIDADMPVIVVAPNNLEKLSKNIIEVRAR 540

Qy 541 GGQLYVFAQQDAGFVSSDNHIIEMPHVEVIAPIFYTVPLQLLAYHVALIKGTVDQPR 600
Db 541 GGQLYVFAQQDAGFVSSDNHIIEMPHVEVIAPIFYTVPLQLLAYHVALIKGTVDQPR 600

Db 541 GGQLYVFAQQDAGFVSSDNHIIEMPHVEVIAPIFYTVPLQLLAYHVALIKGTVDQPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 10
US-10-612-779-12
; Sequence 12, Application US/10612779
; Publication NO. US20040091976A1
; GENERAL INFORMATION:
; APPLICANT: Deng, Ming-De
; APPLICANT: Angerer, J. David
; APPLICANT: Cyron, Don
; APPLICANT: Grund, Alan
; APPLICANT: Jerrell Jr., Thomas
; APPLICANT: Leanna, Candice
; APPLICANT: Mathre, Owen
; APPLICANT: Rosson, Reinhardt
; APPLICANT: Running, Jeff
; APPLICANT: Severson, Dave
; APPLICANT: Song, Linsheng
; APPLICANT: Wassink, Sarah
; TITLE OF INVENTION: Process and Materials for Production of Glucosamine and N-Acetyls
; FILE REFERENCE: 3161-18-2
; CURRENT APPLICATION NUMBER: US/10/612,779
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: 60/393,348
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-612-779-12

Query Match 99.8%; Score 3080; DB 4; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.5e-248;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQAORDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRRLRGKVMQLAAAE 60
Db 1 MCGIVGAIQAORDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRRLRGKVMQLAAAE 60

Qy 61 EPHLGCGTGAIAHTRWATHGPESEVNAHPHVSEHIVVHNGIIEHHEPLREELKARGYTFV 120
Db 61 EPHLGCGTGAIAHTRWATHGPESEVNAHPHVSEHIVVHNGIIEHHEPLREELKARGYTFV 120

Qy 121 SETDTEVIAHLVNMWELKQGGTLREAVLRAIPQURGAYGTVMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNMWELKQGGTLREAVLRAIPQURGAYGTVMDSRHPDTLLAARSGSPLV 180

Qy 181 IGLGMENFIASDQALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKQDIESNLQ 240
Db 181 IGLGMENFIASDQALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKQDIESNLQ 240

Qy 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADLLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADLLSKVEHIQILA 300

Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFEFRYKSAVRNSLMITLSQSGETADTLAGL 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFEFRYKSAVRNSLMITLSQSGETADTLAGL 360

Qy 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQTLTVLLMLVAKL 420
Db 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQTLTVLLMLVAKL 420

Qy 421 SRLKGLDASTEHIDVHGLQALPSRIEOMLSQDKRIEALAEFSDKHAFILGRGQDYPYA 480
Db 421 SRLKGLDASTEHIDVHGLQALPSRIEOMLSQDKRIEALAEFSDKHAFILGRGQDYPYA 480

Db 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSDOKRIEALAEDFSOKHHALFLSRGQDVPJA 480
Qy 481 LEGALKLKEISYIHAEAYAAGELKHGPLALIDADMPVIVVAPNNLELEKLSNIEEVRAR 540
Db 481 LEGALKLKEISYIHAEAYAAGELKHGPLALIDADMPVIVVAPNNLELEKLSNIEEVRAR 540
Qy 541 GGQLYVPADQAGFVSSDNMHIIEMPHVEEVIAPIFVTPVLPQLLAYHVHVALIKGTDVQDPR 600
Db 541 GGQLYVPADQAGFVSSDNMHIIEMPHVEEVIAPIFVTPVLPQLLAYHVHVALIKGTDVQDPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609
RESULT 11
US-10-024-460-25
; Sequence 25, Application US/10024460
; Publication No. US20030044939A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/10/024,460
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 25
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-024-460-25
Query Match 99.8%; Score 3079; DB 4; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.8e-248;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MCGIVGAIAORDVAEILLEGRLRLLEYRGYDSAGLAVVDAGHMTLRRLRGKVOMLAQAAE 60
Db 1 MCGIVGAIAORDVAEILLEGRLRLLEYRGYDSAGLAVVDAGHMTLRRLRGKVOMLAQAAE 60
Qy 61 EPHLHGCGTGAHTRWATHGSPSEVNAHPHVSEHIVVHNGIENHEPLREBELKARGYTFV 120
Db 61 EPHLHGCGTGAHTRWATHGSPSEVNAHPHVSEHIVVHNGIENHEPLREBELKARGYTFV 120
Qy 121 SETDTEVIAHLVNWELKQGGLTLEAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGLTLEAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPLV 180
Qy 181 IGLGMGFNTASDQALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRODIESNLQ 240
Db 181 IGLGMGFNTASDQALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRODIESNLQ 240
Qy 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGNADLLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGNADLLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNSLMITLSQSGETADTLA 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNSLMITLSQSGETADTLA 360
Qy 361 RLSKELGYLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFQTTLTLLMLVAKL 420
Db 361 RLSKELGYLSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFQTTLTLLMLVAKL 420
Qy 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSDOKRIEALAEDFSOKHHALFLGRGQDVPJA 480

Db 421 SRLKGLDASIEHDIHVHGLQALPSRIEQMLSDOKRIEALAEDFSOKHHALFLGRGQDVPJA 480
Qy 481 LEGALKLKEISYIHAEAYAAGELKHGPLALIDADMPVIVVAPNNLELEKLSNIEEVRAR 540
Db 481 LEGALKLKEISYIHAEAYAAGELKHGPLALIDADMPVIVVAPNNLELEKLSNIEEVRAR 540
Qy 541 GGQLYVPADQAGFVSSDNMHIIEMPHVEEVIAPIFVTPVLPQLLAYHVHVALIKGTDVQDPR 600
Db 541 GGQLYVPADQAGFVSSDNMHIIEMPHVEEVIAPIFVTPVLPQLLAYHVHVALIKGTDVQDPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609
RESULT 12
US-10-612-779-8
; Sequence 8, Application US/10612779
; Publication No. US20040091976A1
; GENERAL INFORMATION:
; APPLICANT: Deng, Ming-De
; APPLICANT: Angerer, J. David
; APPLICANT: Cyron, Don
; APPLICANT: Grund, Alan
; APPLICANT: Jerrell Jr., Thomas
; APPLICANT: Leanna, Candice
; APPLICANT: Mathre, Owen
; APPLICANT: Rosson, Reinhardt
; APPLICANT: Running, Jeff
; APPLICANT: Severson, Dave
; APPLICANT: Song, Linsheng
; APPLICANT: Massink, Sarah
; TITLE OF INVENTION: Process and Materials for Production of Glucosamine
; FILE REFERENCE: 3161-18-2
; CURRENT APPLICATION NUMBER: US/10/612,779
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: 60/393,348
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-612-779-8
Query Match 99.8%; Score 3079; DB 4; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.8e-248;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MCGIVGAIAORDVAEILLEGRLRLLEYRGYDSAGLAVVDAGHMTLRRLRGKVOMLAQAAE 60
Db 1 MCGIVGAIAORDVAEILLEGRLRLLEYRGYDSAGLAVVDAGHMTLRRLRGKVOMLAQAAE 60
Qy 61 EPHLHGCGTGAHTRWATHGSPSEVNAHPHVSEHIVVHNGIENHEPLREBELKARGYTFV 120
Db 61 EPHLHGCGTGAHTRWATHGSPSEVNAHPHVSEHIVVHNGIENHEPLREBELKARGYTFV 120
Qy 121 SETDTEVIAHLVNWELKQGGLTLEAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGLTLEAVLRAIPQLRGAYGTVMDSRHPDITLLAARSGSPLV 180
Qy 181 IGLGMGFNTASDQALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRODIESNLQ 240
Db 181 IGLGMGFNTASDQALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRODIESNLQ 240
Qy 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGNADLLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGNADLLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNSLMITLSQSGETADTLA 360

Db 301 CGTSYNGMVSRYPFESLAGIPCDVEIASSEPRYKSAVRNLSMLITLSQGETADTLA 360
QY 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQTLTVLLMLVAKL 420
Db 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQTLTVLLMLVAKL 420
QY 421 SRLKGLDASIEHDI VHGLQALPSRIEQMLSDQKRIEALAEFSDKHHLFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDI VHGLQALPSRIEQMLSDQKRIEALAEFSDKHHLFLGRGDQYPIA 480
QY 481 LEGALKLKEISYIHAEYAAGELKHGPLALIDAMPVIVVAPNNLEKLSNIEEVRAR 540
Db 481 LEGALKLKEISYIHAEYAAGELKHGPLALIDAMPVIVVAPNNLEKLSNIEEVRAR 540
QY 541 GGQLYVPADQAGFVSSDNMHIIEMPHVEEVIAPFYTVPLQLLAYHVALIKGTVDQPR 600
Db 541 GGQLYVPADQAGFVSSDNMHIIEMPHVEEVIAPFYTVPLQLLAYHVALIKGTVDQPR 600
QY 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 13

US-10-024-460-19
; Sequence 19, Application US/10024460
; Publication No. US20030044939A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millie, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/10/024,460
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-024-460-19

Query Match 99.5%; Score 3071; DB 4; Length 609;
Best Local Similarity 99.5%; Pred. No. 8.5e-248;
Matches 606; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MCGTVGAIAQRDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRLGKQVQLAAQAE 60
Db 1 MCGTVGAIAQRDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRLGKQVQLAAQAE 60
QY 61 EPHLHGCTGTAHTRWATHGEPSEVNAPHVSEHIVVHNGIIEHNEPLREELKARGYTFV 120
Db 61 EPHLHGCTGTAHTRWATHGEPSEVNAPHVSEHIVVHNGIIEHNEPLREELKARGYTFV 120
QY 121 SETDTEVIAHLVNWELKQGTLREAVLRAIPQLRGAYGTIVMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGTLREAVLRAIPQLRGAYGTIVMDSRHPDTLLAARSGSPLV 180
QY 181 IGLGMENFTASDQLALLPVTRRFIFLEEGDIAETIRRSVNI FDKTGAEVKRQDIESNLQ 240
Db 181 IGLGMENFTASDQLALLPVTRRFIFLEEGDIAETIRRSVNI FDKTGAEVKRQDIESNLQ 240
QY 241 YDAGDKGIVRHYMOKIIEYQPNNAIKNTLTGRTSHGQVDISELCPNADELLSKVEHIQILA 300
Db 241 YDAGDKGIVRHYMOKIIEYQPNNAIKNTLTGRTSHGQVDISELCPNADELLSKVEHIQILA 300
QY 301 CGTSYNGMVSRYPFESLAGIPCDVEIASSEPRYKSAVRNLSMLITLSQGETADTLA 360

Db 301 CGTSYNGMVSRYPFESLAGIPCDVEIASSEPRYKSAVRNLSMLITLSQGETADTLA 360
QY 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQTLTVLLMLVAKL 420
Db 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQTLTVLLMLVAKL 420
QY 421 SRLKGLDASIEHDI VHGLQALPSRIEQMLSDQKRIEALAEFSDKHHLFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDI VHGLQALPSRIEQMLSDQKRIEALAEFSDKHHLFLGRGDQYPIA 480
QY 481 LEGALKLKEISYIHAEYAAGELKHGPLALIDAMPVIVVAPNNLEKLSNIEEVRAR 540
Db 481 LEGALKLKEISYIHAEYAAGELKHGPLALIDAMPVIVVAPNNLEKLSNIEEVRAR 540
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Db 541 GGQLYVPADQAGFVSSDNMHIIEMPHVEEVIAPFYTVPLQLLAYHVALIKGTVDQPR 600
QY 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 14

US-10-612-779-4
; Sequence 4, Application US/10612779
; Publication No. US20040091976A1
; GENERAL INFORMATION:
; APPLICANT: Deng, Ming-De
; APPLICANT: Angerer, J. David
; APPLICANT: Cyron, Don
; APPLICANT: Grund, Alan
; APPLICANT: Jerrell Jr., Thomas
; APPLICANT: Leanna, Candice
; APPLICANT: Mathre, Owen
; APPLICANT: Rosson, Reinhardt
; APPLICANT: Running, Jeff
; APPLICANT: Severson, Dave
; APPLICANT: Song, Linsheng
; APPLICANT: Wassink, Sarah
; TITLE OF INVENTION: Process and Materials for Production of Glucosamine
; FILE REFERENCE: 3161-18-2
; CURRENT APPLICATION NUMBER: US/10/612,779
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: 60/393,348
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-612-779-4

Query Match 99.5%; Score 3071; DB 4; Length 609;
Best Local Similarity 99.5%; Pred. No. 8.5e-248;
Matches 606; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MCGTVGAIAQRDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRLGKQVQLAAQAE 60
Db 1 MCGTVGAIAQRDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTLRLRLGKQVQLAAQAE 60
QY 61 EPHLHGCTGTAHTRWATHGEPSEVNAPHVSEHIVVHNGIIEHNEPLREELKARGYTFV 120
Db 61 EPHLHGCTGTAHTRWATHGEPSEVNAPHVSEHIVVHNGIIEHNEPLREELKARGYTFV 120
QY 121 SETDTEVIAHLVNWELKQGTLREAVLRAIPQLRGAYGTIVMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGTLREAVLRAIPQLRGAYGTIVMDSRHPDTLLAARSGSPLV 180
QY 181 IGLGMENFTASDQLALLPVTRRFIFLEEGDIAETIRRSVNI FDKTGAEVKRQDIESNLQ 240

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Db 241 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSSELGNADLLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNLSMITLSQSGETADTLA 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNLSMITLSQSGETADTLA 360
Qy 361 RLSKELGYLGS LAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQTLVLLMLVAKL 420
Db 361 RLSKELGYLGS LAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQTLVLLMLVAKL 420
Qy 421 SRLKGLDASTIEHDI VHGLQALPSRIEQMLSDQKRIEALAEFSDKHALFLRGDOVPIA 480
Db 421 SRLKGLDASTIEHDI VHGLQALPSRIEQMLSDQKRIEALAEFSDKHALFLRGDOVPIA 480
Qy 481 LEGALKLKEISYTHAEAYAAGELKHGFLALIDADMPVIVVAPNNELLEKLKSNIEEVRAR 540
Db 481 LEGALKLKEISYTHAEAYAAGELKHGFLALIDADMPVIVVAPNNELLEKLKSNIEEVRAR 540
Qy 541 GGOLYVPADQDAGFVSSDNHIIEMPHVEEVIAPIFVTPVQLLAYHVALIKGTDVDDQPR 600
Db 541 GGOLYVPADQDAGFVSSDNHIIEMPHVEEVIAPIFVTPVQLLAYHVALIKGTDVDDQPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 15
US-10-024-460-22
; Sequence 22, Application US/10024460
; Publication No. US20030044939A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; CURRENT APPLICATION NUMBER: US/10/024,460
; FILE REFERENCE: 3161-18-C1
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-024-460-22

Query Match 99.4%; Score 3068; DB 4; Length 609;
Best Local Similarity 99.5%; Pred. No. 1.5e-247;
Matches 606; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MCGIVGAIQRDVAEILLEGRLREYRGYDSAGLAVVDAEGHMTLRRLRGKVQMLAQAAE 60
Db 1 MCGIVGAIQRDVAEILLEGRLREYRGYDSAGLAVVDTTEGHMTLRRLRGKVQMLAQAAE 60
Qy 61 EHPHGGGTGIAHTRWATHGPSEVNAPHVSEHIVVHNGIIEHHEPLREELKARGYTFV 120
Db 61 EHPHGGGTGIAHTRWATHGPSEVNAPHVSEHIVVHNGIIEHHEPLREELKARGYTFV 120
Qy 121 SETDTEVIAHLVNWELKQGGTLREAVLRATPOLRGAYGTVMDSRHPDTLAARSGPLV 180
Db 121 SETDTEVIAHLVNWELKQGGTLREAVLRATPOLRGAYGTVMDSRHPDTLAARSGPLV 180
Qy 181 IGLGMGNFIASDQLALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKQDIESNLQ 240
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Db 181 IGLGMGNFIASDQLALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKQDIESNLQ 240
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Db 241 YDAGDKGIYRHYMQKEIYEOPNAIKNTLTGRISHGQVDLSSELGNADLLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNLSMITLSQSGETADTLA 360
Db 301 CGTSYNSGMVSRVWFESLAGIPCDVEIASFPRYKSAVRNLSMITLSQSGETADTLA 360
Qy 361 RLSKELGYLGS LAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQTLVLLMLVAKL 420
Db 361 RLSKELGYLGS LAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFPTTQTLVLLMLVAKL 420
Qy 421 SRLKGLDASTIEHDI VHGLQALPSRIEQMLSDQKRIEALAEFSDKHALFLRGDOVPIA 480
Db 421 SRLKGLDASTIEHDI VHGLQALPSRIEQMLSDQKRIEALAEFSDKHALFLRGDOVPIA 480
Qy 481 LEGALKLKEISYTHAEAYAAGELKHGFLALIDADMPVIVVAPNNELLEKLKSNIEEVRAR 540
Db 481 LEGALKLKEISYTHAEAYAAGELKHGFLALIDADMPVIVVAPNNELLEKLKSNIEEVRAR 540
Qy 541 GGOLYVPADQDAGFVSSDNHIIEMPHVEEVIAPIFVTPVQLLAYHVALIKGTDVDDQPR 600
Db 541 GGOLYVPADQDAGFVSSDNHIIEMPHVEEVIAPIFVTPVQLLAYHVALIKGTDVDDQPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609
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Search completed: August 7, 2006, 09:28:24
Job time : 95 secs

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OM protein - protein search, using sw model

Run on: August 7, 2006, 09:27:53 ; Search time 156 Seconds
(without alignments)
261.222 Million cell updates/sec

Title: US-10-612-779-2

Perfect score: 3086

Sequence: 1 MCGIVGAIAGQDVAEILLEG.....LIRGTDVDPNRLAKSVTVE 609

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 236815 seqs, 66914042 residues

Total number of hits satisfying chosen parameters: 236815

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications_AA_New:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	3086	100.0	609	7	US-11-245-473-16 Sequence 16, Appl
2	3080	99.8	609	7	US-11-245-473-28 Sequence 28, Appl
3	3080	99.8	609	7	US-11-245-473-31 Sequence 31, Appl
4	3079	99.8	609	7	US-11-245-473-25 Sequence 25, Appl
5	3071	99.5	609	7	US-11-245-473-19 Sequence 19, Appl
6	3068	99.4	609	7	US-11-245-473-22 Sequence 22, Appl
7	1150	37.3	601	6	US-10-471-571A-2268 Sequence 2268, Ap
8	1109	35.9	681	6	US-10-480-021-6 Sequence 6, Appli
9	1109	35.9	681	6	US-10-480-021-7 Sequence 7, Appli
10	1103.5	35.8	682	6	US-10-480-021-8 Sequence 8, Appli
11	1089.5	35.3	680	6	US-10-953-349-34174 Sequence 34174, A
12	1078	34.9	697	6	US-10-449-902-38427 Sequence 38427, A
13	808	26.2	491	6	US-10-953-349-34175 Sequence 34175, A
14	807	26.2	488	6	US-10-953-349-34176 Sequence 34176, A
15	589.5	19.1	464	6	US-10-488-015-17 Sequence 17, Appl
16	557.5	18.1	286	6	US-10-449-902-36965 Sequence 36965, A
17	252	8.2	541	6	US-10-449-902-54059 Sequence 54059, A
18	240	7.8	501	6	US-10-471-571A-5078 Sequence 5078, Ap
19	222.5	7.2	563	7	US-11-330-403-6080 Sequence 6080, Ap
20	188.5	6.1	600	6	US-10-449-902-38704 Sequence 38704, A
21	186	6.0	541	7	US-11-330-403-13759 Sequence 13759, A
22	186	6.0	544	7	US-11-330-403-6869 Sequence 6869, Ap
23	184.5	6.0	78	6	US-10-488-015-16 Sequence 16, Appl
24	183.5	5.9	610	7	US-11-330-403-1786 Sequence 1786, Ap
25	183	5.9	525	7	US-11-330-403-17502 Sequence 17502, A

ALIGNMENTS

RESULT 1

US-11-245-473-16
; Sequence 16, Application US/11245473
; Publication No. US20060094085A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Mullis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/11/245,473
; CURRENT FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US/10/024,460
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-245-473-16

Query Match 100.0%; Score 3086; DB 7; Length 609;
Best Local Similarity 100.0%; Pred. No. 9.8e-221;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MCGIVGAIAGQDVAEILLEGRLRLEVRGYSAGLAVVDAEGHMTLRRLRGLKQVOMLAQAAE	60
Db	1	MCGIVGAIAGQDVAEILLEGRLRLEVRGYSAGLAVVDAEGHMTLRRLRGLKQVOMLAQAAE	60
Qy	61	EHLHGGTGTAHTRWATHGPESEVNAHPVSEHVVVHNGIIEHNEPLREELKARGYTFV	120
Db	61	EHLHGGTGTAHTRWATHGPESEVNAHPVSEHVVVHNGIIEHNEPLREELKARGYTFV	120
Qy	121	SETDTEVIAHLVNWELKQGGTLREAVLRALPOLRGAYGTVMDSRHPDILLARSGSPLV	180
Db	121	SETDTEVIAHLVNWELKQGGTLREAVLRALPOLRGAYGTVMDSRHPDILLARSGSPLV	180
Qy	181	IGLGMENFTASDQALLPVTRRFIFLEEGDIAETRRSVNIPDKTCAEVKRDIESNLQ	240
Db	181	IGLGMENFTASDQALLPVTRRFIFLEEGDIAETRRSVNIPDKTCAEVKRDIESNLQ	240
Qy	241	YDAGDKGIYRHYMKQEIYEQPNAIKNTLTGRISGHGVDSLSELPNADLLSKVEHIQILA	300
Db	241	YDAGDKGIYRHYMKQEIYEQPNAIKNTLTGRISGHGVDSLSELPNADLLSKVEHIQILA	300

Db 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSLGPNADELLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRYPFESLAGIPCDVEIASSEPRYKSAVRNLSMITLSQGETADTLAAGL 360
Db 301 CGTSYNSGMVSRYPFESLAGIPCDVEIASSEPRYKSAVRNLSMITLSQGETADTLAAGL 360
Qy 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFITQTLTVLLMLVAKL 420
Db 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFITQTLTVLLMLVAKL 420
Qy 421 SRLKGLDASIEHDIYHGLQALPSRIEQMLSDQKRIEALAEFSDKHALFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDIYHGLQALPSRIEQMLSDQKRIEALAEFSDKHALFLGRGDQYPIA 480
Qy 481 LEGALKLKEISYIHAEEYAAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEEVRRAR 540
Db 481 LEGALKLKEISYIHAEEYAAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEEVRRAR 540
Qy 541 GGQLYVFPADQAGFVSSDNMHIEMPHVEEVIAPFIVTVPQLLAYHVALIKGTVDVQDPR 600
Db 541 GGQLYVFPADQAGFVSSDNMHIEMPHVEEVIAPFIVTVPQLLAYHVALIKGTVDVQDPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 2
US-11-245-473-28
; Sequence 28, Application US/11245473
; Publication No. US20060094085A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/11/245,473
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US/10/024,460
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 28
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-245-473-28

Query Match 99.8%; Score 3080; DB 7; Length 609;
Best Local Similarity 99.8%; Pred. No. 2.7e-220;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIAQRDVAAEILLEGRLREYRGYDSAGLAVVDAEGHMTLRRLRGKVQMLAQAAE 60
Db 1 MCGIVGAIAQRDVAAEILLEGRLREYRGYDSAGLAVVDAEGHMTLRRLRGKVQMLAQAAE 60
Qy 61 EHPHGGTGIAHTRWATHGEPSEVNAPHVSEHIVVHNGIIEHNEPLREELKARGYTFV 120
Db 61 EHPHGGTGIAHTRWATHGEPSEVNAPHVSEHIVVHNGIIEHNEPLREELKARGYTFV 120
Qy 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPOLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPOLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Qy 181 IGLGMGENFTASDQALLPVTRRFIFLEEGDIAETITRRSVNIFDKTGAEVKQDIESNLQ 240
Db 181 IGLGMGENFTASDQALLPVTRRFIFLEEGDIAETITRRSVNIFDKTGAEVKQDIESNLQ 240

Qy 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSLGPNADELLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSLGPNADELLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRYPFESLAGIPCDVEIASSEPRYKSAVRNLSMITLSQGETADTLAAGL 360
Db 301 CGTSYNSGMVSRYPFESLAGIPCDVEIASSEPRYKSAVRNLSMITLSQGETADTLAAGL 360
Qy 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFITQTLTVLLMLVAKL 420
Db 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFITQTLTVLLMLVAKL 420
Qy 421 SRLKGLDASIEHDIYHGLQALPSRIEQMLSDQKRIEALAEFSDKHALFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDIYHGLQALPSRIEQMLSDQKRIEALAEFSDKHALFLGRGDQYPIA 480
Qy 481 LEGALKLKEISYIHAEEYAAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEEVRRAR 540
Db 481 LEGALKLKEISYIHAEEYAAGELKHGPLALIDAMPVIVVAPNNELLEKLKSNIEEVRRAR 540
Qy 541 GGQLYVFPADQAGFVSSDNMHIEMPHVEEVIAPFIVTVPQLLAYHVALIKGTVDVQDPR 600
Db 541 GGQLYVFPADQAGFVSSDNMHIEMPHVEEVIAPFIVTVPQLLAYHVALIKGTVDVQDPR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 3
US-11-245-473-31
; Sequence 31, Application US/11245473
; Publication No. US20060094085A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/11/245,473
; PRIOR FILING DATE: 2005-10-05
; PRIOR APPLICATION NUMBER: US/10/024,460
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 31
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-245-473-31

Query Match 99.8%; Score 3080; DB 7; Length 609;
Best Local Similarity 99.8%; Pred. No. 2.7e-220;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MCGIVGAIAQRDVAAEILLEGRLREYRGYDSAGLAVVDAEGHMTLRRLRGKVQMLAQAAE 60
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Qy 61 EHPHGGTGIAHTRWATHGEPSEVNAPHVSEHIVVHNGIIEHNEPLREELKARGYTFV 120
Db 61 EHPHGGTGIAHTRWATHGEPSEVNAPHVSEHIVVHNGIIEHNEPLREELKARGYTFV 120
Qy 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPOLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPOLRGAYGTVMDSRHPDTLLAARSGSPLV 180
Qy 181 IGLGMGENFTASDQALLPVTRRFIFLEEGDIAETITRRSVNIFDKTGAEVKQDIESNLQ 240
Db 181 IGLGMGENFTASDQALLPVTRRFIFLEEGDIAETITRRSVNIFDKTGAEVKQDIESNLQ 240

Db 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVIMDSRHPDTLLAARSGSPLV 180
Qy 181 IGLGNGFNFIASDQALLPVTTRRFIFLEEGDIAETIRRSVNI FDKTGAEVKQDIESNLQ 240
Db 181 IGLGNGFNFIASDQALLPVTTRRFIFLEEGDIAETIRRSVNI FDKTGAEVKQDIESNLQ 240
Qy 241 YDAGDKGIYRHYMQKEIYEQNAIKNTLTGRISHGQVDLSLGNADLLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEQNAIKNTLTGRISHGQVDLSLGNADLLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRYPFESLAGIPCDVEIASFPRYKSAVRNSLMTITLSQSGTADTLA 360
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Qy 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQTLVLLMLVAKL 420
Db 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQTLVLLMLVAKL 420
Qy 421 SRLKGLDASIEHDI VHGLQALPSRIEQMLSDKRTEALAEFSDKXHALFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDI VHGLQALPSRIEQMLSDKRTEALAEFSDKXHALFLGRGDQYPIA 480
Qy 481 LEGALKLKEISYIHAEEYAAAGELKHGPIALIDAMPVIVVAPNNELLEKLKSNIEEVRAR 540
Db 481 LEGALKLKEISYIHAEEYAAAGELKHGPIALIDAMPVIVVAPNNELLEKLKSNIEEVRAR 540
Qy 541 GGQLYVFADQDAGFVSSDNMHIEMPHVEEVIAPFYFTVPLQLLAYHVALIKGTDVQDR 600
Db 541 GGQLYVFADQDAGFVSSDNMHIEMPHVEEVIAPFYFTVPLQLLAYHVALIKGTDVQDR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 6

US-11-245-473-22
; Sequence 22, Application US/11245473
; Publication No. US20060094085A1
; GENERAL INFORMATION:
; APPLICANT: Berry, Alan
; APPLICANT: Burlingame, Richard P.
; APPLICANT: Millis, James R.
; TITLE OF INVENTION: PROCESS AND MATERIALS FOR PRODUCTION OF GLUCOSAMINE
; FILE REFERENCE: 3161-18-C1
; CURRENT APPLICATION NUMBER: US/11/245,473
; CURRENT FILING DATE: 2005-10-05
; PRIOR FILING DATE: 2001-12-17
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/115,475
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-15
; PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 60/035,494
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 609
; TYPE: PRT
; ORGANISM: Escherichia coli
US-11-245-473-22

Query Match 99.4%; Score 3068; DB 7; Length 609;
Best Local Similarity 99.5%; Pred. No. 2.1e-219;
Matches 606; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MCGIVGAIAQRDVAEILLGLRLRYRGYDSAGLAVVDAGHMTLRRLRGKVMQMLAAQAE 60
Db 1 MCGIVGAIAQRDVAEILLGLRLRYRGYDSAGLAVVDAGHMTLRRLRGKVMQMLAAQAE 60
Qy 61 EHPHGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIENHEPRLREELKARGYTFV 120
Db 61 EHPHGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIENHEPRLREELKARGYTFV 120

Qy 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVIMDSRHPDTLLAARSGSPLV 180
Db 121 SETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVIMDSRHPDTLLAARSGSPLV 180
Qy 181 IGLGNGFNFIASDQALLPVTTRRFIFLEEGDIAETIRRSVNI FDKTGAEVKQDIESNLQ 240
Db 181 IGLGNGFNFIASDQALLPVTTRRFIFLEEGDIAETIRRSVNI FDKTGAEVKQDIESNLQ 240
Qy 241 YDAGDKGIYRHYMQKEIYEQNAIKNTLTGRISHGQVDLSLGNADLLSKVEHIQILA 300
Db 241 YDAGDKGIYRHYMQKEIYEQNAIKNTLTGRISHGQVDLSLGNADLLSKVEHIQILA 300
Qy 301 CGTSYNSGMVSRYPFESLAGIPCDVEIASFPRYKSAVRNSLMTITLSQSGTADTLA 360
Db 301 CGTSYNSGMVSRYPFESLAGIPCDVEIASFPRYKSAVRNSLMTITLSQSGTADTLA 360
Qy 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQTLVLLMLVAKL 420
Db 361 RLSKELGYLGSIAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQTLVLLMLVAKL 420
Qy 421 SRLKGLDASIEHDI VHGLQALPSRIEQMLSDKRTEALAEFSDKXHALFLGRGDQYPIA 480
Db 421 SRLKGLDASIEHDI VHGLQALPSRIEQMLSDKRTEALAEFSDKXHALFLGRGDQYPIA 480
Qy 481 LEGALKLKEISYIHAEEYAAAGELKHGPIALIDAMPVIVVAPNNELLEKLKSNIEEVRAR 540
Db 481 LEGALKLKEISYIHAEEYAAAGELKHGPIALIDAMPVIVVAPNNELLEKLKSNIEEVRAR 540
Qy 541 GGQLYVFADQDAGFVSSDNMHIEMPHVEEVIAPFYFTVPLQLLAYHVALIKGTDVQDR 600
Db 541 GGQLYVFADQDAGFVSSDNMHIEMPHVEEVIAPFYFTVPLQLLAYHVALIKGTDVQDR 600
Qy 601 NLAKSVTVE 609
Db 601 NLAKSVTVE 609

RESULT 7

US-10-471-571A-2268
; Sequence 2268, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2268
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-471-571A-2268

Query Match 37.3%; Score 1150; DB 6; Length 601;
Best Local Similarity 40.8%; Pred. No. 3.2e-77;
Matches 252; Conservative 126; Mismatches 214; Indels 26; Gaps 10;

Qy 1 MCGIVGAIAQRDVAEILLGLRLRYRGYDSAGLAVVDAGHMTLRRLRGKVMQMLAAQAE 60
Db 1 MCGIVGAIAQRDVAEILLGLRLRYRGYDSAGLAVVDAGHMTLRRLRGKVMQMLAAQAE 59
Qy 61 EHPHGGTGIAHTRWATHGEPSEVNAHPVSEHIVVHNGIENHEPRLREELKARGYTFV 118
Db 60 SSDPDGVPVIGHTRWATHGVNHNHSHPHQSSNGRFTLVHNGVIENYEELKGEY-LQGV 118
Qy 119 FVSETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVIMDSRHPDTLLAARSGSP 178
Db 119 FVSETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVIMDSRHPDTLLAARSGSP 178

179	Qy	LVI	G	L	G	W	G	E	N	F	I	A	S	D	I	A	L	L	P	V	T	R	R	F	I	F	L	E	B	G	I	A	E	I	T	R	S	V	N	I	F	D	K	T	G	A	E	V	K	R	O	D	I	E	S	N	238					
179	Db	LL	G	V	G	E	F	N	V	I	A	S	D	A	L	A	M	L	O	V	T	S	E	Y	K	E	I	H	D	E	I	V	I	V	K	K	D	E	V	I	I	K	D	A	D	G	N	V	V	E	R	D	S	I	A	E	238					
239	Qy	L	O	V	D	A	G	K	G	I	R	H	Y	M	O	K	E	I	Y	O	P	N	A	I	K	N	T	L	---	T	G	R	I	S	H	G	O	V	D	L	S	E	L	G	P	N	A	D	E	L	L	K	292									
239	Db	I	D	A	S	D	A	K	G	V	Y	A	H	Y	M	L	K	E	I	H	O	P	A	M	R	I	I	O	E	Y	O	D	A	E	G	N	L	K	I	D	O	I	I	N	---	V	K	E	290													
293	Qy	V	E	H	I	O	I	A	C	T	S	Y	N	G	M	V	R	Y	W	F	S	L	A	G	I	P	C	D	V	E	I	A	S	E	F	R	Y	K	S	A	V	R	N	S	L	M	I	T	S	O	S	G	E	352								
291	Db	A	D	R	I	Y	I	A	A	G	T	S	Y	H	A	G	L	V	G	K	E	F	L	E	K	A	G	V	P	T	E	V	H	V	A	S	E	F	V	N	M	P	L	S	E	K	P	L	F	V	I	S	O	S	G	E	350					
353	Qy	T	A	D	T	A	G	L	R	L	S	K	E	L	G	S	L	A	I	C	N	P	G	S	S	L	V	R	E	S	D	L	A	M	T	N	A	G	E	I	G	V	A	S	T	K	A	F	T	O	L	T	V	412								
351	Db	T	A	S	R	A	V	L	T	E	N	K	U	G	H	---	K	S	L	T	I	T	I	N	V	A	G	S	T	L	R	E	A	D	H	T	L	L	L	H	A	G	E	I	A	V	A	S	T	K	A	F	T	A	O	I	A	V	409			
413	Qy	L	L	M	V	A	K	L	S	R	L	K	G	L	D	A	S	I	E	H	D	I	V	H	G	L	A	P	S	R	I	E	O	M	L	S	O	D	K	R	I	E	A	L	A	E	D	F	S	D	---	R	H	A	L	F	L	471				
410	Db	L	S	I	L	S	Q	I	V	A	E	K	H	E	G	R	E	A	D	I	---	D	L	L	R	E	L	A	K	V	T	T	A	I	E	A	I	V	D	D	A	P	I	M	E	G	I	A	T	D	F	L	E	T	T	R	N	A	F	F	I	467
472	Qy	G	R	G	O	Y	P	I	A	L	E	G	A	L	K	I	K	E	I	S	I	H	A	E	A	V	A	G	L	K	H	G	L	P	A	L	I	D	A	D	P	V	I	V	A	P	N	N	E	L	L	E	K	L	531							
468	Db	G	R	T	I	D	N	V	N	S	E	G	A	L	K	I	K	E	I	S	I	Q	A	E	F	A	G	G	E	L	G	T	I	A	I	E	B	E	G	F	V	V	G	L	A	T	O	E	K	N	V	N	S	I	R	527						
532	Qy	S	N	T	E	E	V	A	R	G	Q	L	V	F	A	D	O	A	G	F	V	S	S	D	N	M	I	I	E	M	P	H	V	E	E	V	A	P	T	F	Y	T	P	L	O	L	L	A	H	V	A	L	I	591								
528	Db	G	N	V	K	E	V	A	R	G	A	H	P	C	I	I	S	M	E	---	G	L	E	K	E	G	D	T	Y	I	---	P	H	V	E	L	L	T	P	L	V	S	V	A																		

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RESULT 8
US-10-480-021-6
; Sequence 6, Application US/10480021
; Publication No. US20060121457A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: GFATS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-068
; CURRENT APPLICATION NUMBER: US/10/480,021
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-480-021-6

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Qy	151	PQRGAYGVTVIMDSRHPDPTLLAARSGGSPVLVGLGMG-----	186
Db	179	QOLEGAEPALVPKSVHFFPQCAVGTRGRSGPLLIIGVRSEHKLSHDHIPILYRTGDKDGKSGCNL	238
Qy	187	-----ENFTASDOLALLPVTRGFIFLEEGDIAEIT--RSVNIFDKTG	227
Db	239	SRVDSTTCLFPVBKEAVEYYFASDASAVIEHTNRVIPLEDDDVAADVGRLSIHRIKRTA	298
Qy	228	AEVKRQDIESNLQVDAGD--KGIVRRHYMKOEIYEOPNAIKNTLTGRISHGQVDLSBELGEN	285
Db	299	GDFHGRAVQT-LQWELQOIKMGFNSSFMQKEIFEQPESVNVTMRGRNVDPDYTN-VLGL	356
Qy	286	ADEL--LSKVHEHIQILACGTSYNGMWSRYNFESLAGIPCDVEIASEFYRKSAVRRNSL	343
Db	357	KDHIKEIQRCRRLLILIACGTSYHAGVATQVLEELTELPVMVELASDFLDNRNTPVFRDDV	416
Qy	344	MITSQSGETADTTAGRLSKELGYLGSLATCNVPGSSLRVRESDLAMTNAGETGVAST	403
Db	417	CFFLSQSGETADTLMLGRYCKERGAL-TVGITNTVGSISRBTDCGVHINAGPEIGVAST	475
Qy	404	KAFITTOLTVLMLVAKLSRLAGLDASIETHDIVHGILOALPSRIEOMLSODKRITEALAEDFS	463
Db	476	KAYTSQFVSLVFWFALMMCCDDRISMWOERKKEIMUGLKURPDLLIKEVLSMDDEIQKLATELY	535
Qy	464	DKHHALFLRGDQPIALEGALKKEIYSIIHAEEYAAGELKHGPPLIALIDAMPVIWVAPN	523
Db	536	HQKSVLINGRGYHYATCLEGALKIKEYTYMHSEGTLAGELKHGPPLAVDKLMPVIMIINR	595
Qy	524	NELLEKLKSNITEEVARGGQLYVFADQAGFVSSDNMHI IEMPHVEEVIAPIFYTVPQLQ	583
Db	596	DHTYAKQNALQQVVARGRPVVICDEDTETIKNTKRTIKVPHSVDCLOGILSVIPLQL	655
Qy	584	LAYHVALLKGTVDQDPNNLAKSVTVE	609
Db	656	LAFHLAVLRGDYDVDFPRNLAKSVTVE	681

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RESULT 9
US-10-480-021-7
; Sequence 7, Application US/10480021
; Publication No. US20060121457A1
; GENERAL INFORMATION:
; APPLICANT: EXELUXIS, INC.
; TITLE OF INVENTION: GFATs AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-068
; CURRENT APPLICATION NUMBER: US/10/480,021
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 681
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-480-021-7

```


Qy	324	DVEIASEFRYKSAVRNLSMITLSQSGETADTLAGRLSKELGYLGSLAICNVPSSLV	383
Db	306	SVELASDFLDQAPVFEDDTCVFSQSGETADSLMALRYCLERGA	364
Qy	384	RESDLALMTNAGTEIGVASTKAF	443
Db	365	LLTHCGVHINAGPEIGVASTKAYTSQFVAMVFALS	424
Qy	444	RIQMLSQDKRIEAL-AEDFSDKHAF	482
Db	425	QFKEILKLINEPIKOMCAKFFKNOKS	464

Search completed: August 7, 2006, 09:31:32
Job time : 158 secs

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